

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 14:59:16 ; Search time 40 Seconds

(without alignments)
841.251 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATSPGWVINDWPGYDLN.....LDYNEYPDLNHCIVINEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.*

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2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
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8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1116	100.0	212	17 AAR98224	Hypoxanthine guani
2	1069	95.8	225	21 AAY79212	Human transferase
3	1065	95.4	225	22 AAB94995	Human protein sequ
4	1065	95.4	230	23 ABP41467	Human ovarian anti
5	772	69.2	218	18 AAW37339	Mouse HPRT. Mus m
6	445.5	39.9	231	22 AAB85165	P. falciparum HGPR
7	265.5	23.8	180	23 ABB54862	Lactococcus lactis
8	261	23.4	183	23 ABB53319	Lactococcus lactis
9	257.5	23.1	180	23 ABP27993	Streptococcus poly

10	251.5	22.5	194	22 AAG92711	C glutamicum prote
11	251.5	22.5	200	22 AAB80144	Corynebacterium gi
12	250.5	22.4	648	23 ABB47663	Listeria monocytog
13	247.5	22.2	180	19 AAW80653	S. pneumoniae puta
14	247.5	22.2	180	24 ABU02782	S. pneumoniae type
15	245.5	22.0	180	22 AAM01114	CPE 117 protein se
16	243	21.8	58	21 AAG02773	Human secreted pro
17	238.5	21.4	181	23 ABP38473	Staphylococcus epi
18	232.5	20.8	180	23 ABP27992	Streptococcus poly
19	225.5	20.2	187	22 AAU41731	Propionibacterium
20	209.5	18.8	188	21 AAG21927	Arabidopsis thalia
21	209.5	18.8	188	23 ABB91553	Herbicidally activ
22	209.5	18.8	193	21 AAG21926	Arabidopsis thalia
23	208.5	18.7	187	23 ABP66271	Blifidobacterium lo
24	147	13.2	56	21 AAB59068	Breast and ovarian
25	143	12.8	127	23 ABP35009	Human transferase
26	138.5	12.4	200	24 ABP77089	N. gonorrhoeae ami
27	122.5	11.0	173	24 ABU01712	S. pneumoniae type
28	117	10.5	192	22 AAG91529	C glutamicum prote
29	114.5	10.3	173	23 ABP26684	Streptococcus poly
30	113.5	10.2	194	22 AAU51709	Propionibacterium
31	110	9.9	173	23 ABB54950	Lactococcus lactis
32	108.5	9.7	173	23 ABP30396	Streptococcus poly
33	108.5	9.7	185	23 ABP26683	Streptococcus poly
34	103.5	9.3	155	22 AAB96065	Puative P. abyss
35	96	8.6	182	20 AAY06888	S. aureus pyrk hom
36	94	8.4	440	22 ABG15272	Novel human diagno
37	94	8.4	573	22 ABG28703	Novel human diagno
38	91.5	8.2	183	23 ABB47706	Listeria monocytog
39	89	8.0	187	23 ABP39935	Staphylococcus epi
40	88.5	7.9	199	21 AAY74558	Neisseria gonorrhe
41	88.5	7.9	199	21 AAY74560	Neisseria meningit
42	88.5	7.9	199	24 ABP81041	N. gonorrhoeae ami
43	87.5	7.8	199	21 AAY74559	Neisseria meningit
44	87	7.8	494	19 AAW69250	Human p56-2 protei
45	87	7.8	494	21 AAY78948	Human p56-2 amino

ALIGNMENTS

RESULT 1

AAR98224 standard; Protein; 212 AA.

XX AAR98224; (first entry)

DT 24-SEP-1996

XX Hypoxanthine guanine phosphoribosyl transferase 2.

DE Hypoxanthine guanine phosphoribosyl transferase 2; HPRT-2; purine;

KW Lesh-Nyhan syndrome; gout; nephrolithiasis; uricaciduria;

KW nephropathy; anaemia; therapy; agonist; antagonist.

OS Homo sapiens.

XX WO9612501-A1.

PN 02-MAY-1996.

PD 19-OCT-1994; 94WO-US11914.

PF 19-OCT-1994; 94WO-US11914.

PR 03-NOV-1994; 94ZA-0008693.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Bednarik DP, Rosen CA;

PI WPI; 1996-230368/23.

DR N-PSDB; AAT30127.

XX

Db		194 FVVGALDYNEYPFDLNLHCIVINEHG 219	
	RESULT 3		
	AAB94995		
ID	AAB94995 standard; Protein; 225 AA.		
XX			
AC	AAB94995;		
XX			
DT	26-JUN-2001 (first entry)		
XX			
DE	Human protein sequence SEQ ID NO:16623.		
XX			
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy.		
OS	Homo sapiens.		
PB	EP1074617-A2.		
XX			
PD	07-FEB-2001.		
XX			
PF	28-JUL-2000; 2000EP-0116126.		
XX			
PR	29-JUL-1999; 99JP-0248036.		
FR	27-AUG-1999; 99JP-0300253.		
PR	11-JAN-2000; 2000JP-0118776.		
PR	02-MAY-2000; 2000JP-0183767.		
PR	09-JUN-2000; 2000JP-0241899.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX			
DR	WPI; 2001-318749/34.		
XX			
PT	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length cDNAs defined in the specification, and for the detection		
PT	and/or diagnosis of the abnormality of the proteins encoded by the		
PT	full-length cDNAs -		
PS	Claim 8; SEQ ID 16623; 2537pp + CD ROM; English.		
CC	The present invention describes primer sets for synthesising 5602		
CC	full-length cDNAs defined in the specification. Where a primer set		
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary		
CC	to the complementary strand of a polynucleotide which comprises one of		
CC	the 5602 nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	nucleotide and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in		
CC	the specification. The primer sets can be used in antisense therapy and		
CC	in gene therapy. The primers are useful for synthesising polynucleotides,		
CC	particularly full-length cDNAs. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		
CC	the full-length cDNAs. The primers allow obtaining of the full-length		
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and		
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to		
CC	AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632		
CC	represent oligonucleotides, all of which are used in the exemplification		
CC	of the present invention.		
XX			
SQ	Sequence 225 AA;		
	Query Match 95.4%; Score 1065; DB 22; Length 225;		
	Best Local Similarity 98.5%; Pred. No. 9.5e-110;		
	Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
QY	7 GVIMDDWPGYDLNLFETYPOHYGDLLEYVLPHGIIVDRIERAKDMKIDIGYSIDMVLVC 66		

disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 230 AA;
 Query Match 95.4%; Score 1065; DB 23; Length 230;
 Best Local Similarity 98.5%; Pred. No. 9.7e-110;
 Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GVVIMDDPGYDLNLTYPQHYGGDLEVLPHGIIVDRIERIAKDIMKDIGSDIMVLC 66
 Db 19 GVVIMDDPGYDLNLTYPQHYGGDLEVLPHGIIVDRIERIAKDIMKDIGSDIMVLC 78
 QY 67 VLKGGYKFCADLVEHLKNISRSNDRFVSMKVDIFIRLKSYNRQDSMGEMOIIIGGDLSTIA 126
 Db 79 VLKGGYKFCADLVEHLKNISRSNDRFVSMKVDIFIRLKSYNRQDSMGEMOIIIGGDLSTIA 138
 QY 127 GKNFLIVEDVGTGRMTKALLNIEKYKPNMIVKASLLVKRTSRSDGPRPDYAGFEIPLH 186
 Db 139 GRNVLIVEDVGTGRMTKALLNIEKYKPNMIVKASLLVKRTSRSDGPRPDYAGFEIPLH 198
 QY 187 FVVGVALDYNEFRDLNHCIVNEHG 212
 Db 199 FVVGVALDYNEFRDLNHCIVNEHG 224

RESULT 5
 AAW37339
 ID AAW37339 standard; Protein; 218 AA.

XX AAW37339;
 AC AAW37339;
 DT 11-MAY-1998 (first entry)
 XX Mouse HPRT.
 DE
 KW Vaccine, B-cell malignancy; lymphoma; leukaemia; tumour;
 KW gene amplification; immunotherapy; therapy; mouse; HPRT;
 KW hypoxanthine-phosphoribosyltransferase; selectable marker;
 KW vector; pMSD5-HPRT.

OS Mus musculus.

XX WO9741244-A1.

XX 06-NOV-1997.

XX 25-APR-1997; 97WO-US07039.

XX 06-DEC-1996; 96US-0761277.

XX 01-MAY-1996; 96US-0644664.

XX (GENI-) GENITOPE CORP.

XX Denney DW;

XX WPI; 1997-549743/50.

XX N-PSDB; AAT97166.

XX Multivalent vaccine to treat B cell lymphoma or leukaemia -
 PT comprises at least 2 different recombinant variable regions of
 PT immunoglobulin molecules derived from B cell lymphoma cells
 XX
 PS Example 2; Page 108-109; 177pp; English.
 XX
 CC This sequence comprises hypoxanthine phosphoribosyltransferase
 CC (HPRT) from mouse. The HPRT gene (see AAT97166) was utilised in
 CC the construction of selection vector pMSD5-HPRT, which contains
 CC full-length HPRT DNA under transcriptional control of the Moloney
 CC LTR (see also AAT97166). The invention provides vectors and improved
 CC methods for the expression and co-amplification of genes encoding
 CC recombinant proteins in cultured cells. The methods permit the
 CC isolation of cell lines which have co-amplified input recombinant
 CC sequences which encode an amplifiable marker, one or more
 CC expression vectors encoding a protein of interest and optionally a
 CC selectable marker. The amplified cells provide large quantities of
 CC recombinant proteins suitable for immunotherapy for treatment of
 CC lymphomas and leukaemias. The methods permit the production of
 CC custom vaccines, including multivalent vaccines, that reflect the
 CC degree of somatic variation found in a patient's tumour.

XX Sequence 218 AA;

Query Match 69.2%; Score 772; DB 18; Length 218;
 Best Local Similarity 67.9%; Pred. No. 3.1e-77;
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
 QY 1 MATRSPGVIMDDPGYDLNLTYPQHYGGDLEVLPHGIIVDRIERIAKDIMKDIGYS 60
 Db 1 MPTRSPGVISDDPEGYDLDFCIPNHYAEDLEKVFIPHGLIMDRTERLARDVMKEMGGH 60
 QY 61 DIMVLCLVKGKFCADLVEHLKNISRSNDRFVSMKVDIFIRLKSYNRQDSMGEMOIIIGG 120
 Db 61 HIVALCLVKGKFCADLVEHLKNISRSNDRFVSMKVDIFIRLKSYNRQDSMGEMOIIIGG 120
 QY 121 DLSTLAGKNFLIVEDVGTGRMTKALLNIEKYKPNMIVKASLLVKRTSRSDGPRPDYAG 180
 Db 121 DLSTLTGKNVLIVEDIDTGTMTQTLTSLVQKQSPMKVKASLLVKRTSRSGYRDFV 180
 QY 181 FEIPLFVVGVALDYNEFRDLNHCIVNEHG 212
 Db 181 FEIPDKFVVGVALDYNEFRDLNHCIVNEHG 212

RESULT 6
 AAB85165
 ID AAB85165 standard; Protein; 231 AA.

XX AAB85165;
 AC AAB85165;
 DT 07-SEP-2001 (first entry)
 XX P. falciparum HGPRT enzyme.

XX Hypoxanthine-guanine phosphoribosyl transferase; HGPRT; enzyme; malaria;
 KW plasmodium.

XX Plasmodium falciparum.

XX US6248577-B1.

XX 19-JUN-2001.

XX 16-JUL-1990; 90US-0552744.

XX 16-JUL-1990; 90US-0552744.

XX (SOUR) SOUTHERN RES INST.

XX Vasanthakumar G, Montgomery JA;

Claim 17; SEQ ID NO: 6465; 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Corynebacterium glutamicum strain. These sequences are useful for identifying the mutation point of a gene derived from a mutant of corynebacterium glutamicum, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Corynebacterium glutamicum, and identifying a homologue of a gene derived from Corynebacterium glutamicum. Corynebacterium glutamicum is useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.

Query Match 22.5%; Score 251.5; DB 22; Length 194;
Best Local Similarity 34.3%; Pred. No. 1.6e-19;
Matches 69; Conservative 41; Mismatches 68; Indels 23; Gaps 9

Seq Sequence 194 AA;

QY 18 DLNFTYPQHVG-DLEVLPHGILIVDRIFERLAKDIMKDI--GVSDIMVLVCKGGYKF 74
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |
Dd 6 DLNV---PANPYGTDIESLVISEEKLQRIAEAMKRVSSEFKDAEDILVCLVKGAIFY 62
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |
QY 75 CADLVEHLKNTRNSDRFVSMKVDFIRLKSYRND-QSGMEMQIIGGDLSTLAGKNFLIV 133
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |
Dd 63 LAD-----FSRLMD--IPTQSEPMAVSSYGNTSSGGVVRLKDL-KIEGGDVLI 112
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |
QY 134 EDVVTGRTMKALLSNIEKYKPNIKKVASLLVK---RTSRSDGFPRDYAGFEIPLHFWVG 190
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |
Dd 113 EDIIDSGLTSLWMLNKLNRNPKSINVITLLRKPERLTINIDMFD---IGDIPNEFWVG 169
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |
QY 191 YALDINEYFRDLNHICVINEH 211
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |
Dd 170 YGLDFAERYRDLPVVGTLEPH 190
| | | : : : | : | : | : : | : | : | : : | : | : | : | : |

RESULT 11
AAB80144
ID AAB80144 standard; Protein; 200 AA.
XX AC AAB80144;
XX DT 30-APR-2001 (first entry)
XX DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:1022.
XX KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;
KW fine chemical production; microorganism; organic acid; nucleoside;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
XX OS Corynebacterium glutamicum.
XX PN WO200100843-A2.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-IB00923.
XX PR 25-JUN-1999; 99US-0141031.
PR 01-JUL-1999; 99DE-1030476.
PR 02-JUL-1999; 99US-0142101.
PR 08-JUL-1999; 99DE-1031415.
PR 08-JUL-1999; 99DE-1031418.
PR 08-JUL-1999; 99DE-1031419.
PR 08-JUL-1999; 99DE-1031420.
PR 08-JUL-1999; 99DE-1031424.
PR 08-JUL-1999; 99DE-1031428.

Query Match 22.5%; Score 251.5; DB 22; Length 200;
Best Local Similarity 34.3%; Pred. No. 1.7e-19;
Matches 69; Conservative 41; Mismatches 68; Indels 23; Gaps 9;

QY 18 DLNLFYPOHYG-DLEVLPHGIIVDRIERLAKIMKDI--GYSDIMVLCVLKGYKF 74
DB 12 DLNV---PANPYTDIESVLISEKUKQRIAEKAKRSEFEKDAEDLILVLCVLKGAIFY 69

QY 75 CADLVEHLKNIISNRDRFVSMKVDIFRLKSYRND-QSMGEMQIIGGGDLSTLAGKNFLIV 133
DB 69 LAD-----FSRMLD--IPTQSEFNAVSSYGNSTSSGGVIRLKDL-KEIGRDVLIV 118

QY 134 EDVVGTRMTKALLSNIIEKYPNMIKVASLLVK---RTSRSDGRDPDYAGFEIPHFLFVVG 190
DB 119 EDIIDSGLTSLWMLRNLKRNPKSLNVITLLRPERLTTNIDMFD---IGFDIPNEFVVG 175

QY 191 YALDYNEYFRDLNHNICVINEH 211
DB 176 YGLDFAERYRDLFVYGTLEPH 196

RESULT 12
ABB47663
ID ABB47663 standard; Protein; 648 AA.
AC ABB47663;
XX

DT 05-FEB-2002 (first entry)
XX

DE Listeria monocytogenes protein #367.
XX

KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW Vitamin B12; Bacterial infection; disease.
XX

OS Listeria monocytogenes.
XX

PN WO200177335-A2.
XX

PD 18-OCT-2001.
XX

PF 11-APR-2001; 2001WO-FR01118.
XX

PR 11-APR-2000; 2000FR-0004629.
XX

PA (INSP) INST PASTEUR.
XX

PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Biaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX

DR WPI; 2002-010914/01.
XX

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides -
XX

XX Claim 6; SEQ ID No 368; 192pp; French.
PS

CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and related organisms. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin

CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WFO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 648 AA;
Query Match 22.4%; Score 250.5; DB 23; Length 648;
Best Local Similarity 33.0%; Pred. No. 1.1e-18;
Matches 60; Conservative 46; Mismatches 63; Indels 13; Gaps 5;

QY 29 YGDLVVLPHGIIVDRIERLAKIMKDIKIDYSDIMVLCVLKGYKFCADLVEHLKNIISRN 88
DB 471 HNDIQVLISEDELQEKIRELGTTEYGRNPLVGVVLKGATPFMTDLKRV----- 524

QY 89 SDRFVSMKVDIFRLKSYRNDQ-SMGEMQIIGGGDL-STLAGKNFLIVEDVVGTRMTKAL 146
DB 525 -DTYLEM--DFMDVSSYGNSTSSGGEVKII--KDLNASVEGRDVLVIEDIISGRTLSYL 579

QY 147 LSNIEKYKPNMIKVASLLVKTSSRSDGRDPDYAGFEIPHFLFVVGALDYNEYFRDLNHNIC 206
DB 580 VDLIKYRKAKSVKLVTLDDKPAGRNVEIADYVGVVVPNEFVVGGLDYAERYNLPYIG 639

QY 207 VI 208
DB 640 IL 641

RESULT 13
AAW80653
ID AAW80653 standard; Protein; 180 AA.
XX
AC AAW80653;
XX

DT 24-DEC-1998 (first entry)
XX

DE S. pneumoniae putative ATPase involved in membrane functions.
XX

KW Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
KW virulence; antibody; infection; detection; treatment; hypothetical;
KW cell wall biosynthetic, external target; minimal gene set protein.
XX

OS Streptococcus pneumoniae.
XX

XX WO9826072-A1.
XX

PD 18-JUN-1998.
XX

PF 09-DEC-1997; 97WO-US22578.
XX

PR 13-DEC-1996; 96US-0036281.
XX

PA (ELIL) LILLY & CO ELI.
XX

PI Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;
PI Mills BJ, Norris FH, Peery RB, Rockey PK, Rostock PR;
PI Skatrud PL, Smith MC, Solenberg PJ, Treadway PJ;
PI Young Bellido ML;
XX

DR WPI; 1998-348529/30.
DR N-PSDB; AAV65227.
XX

PT Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
PT for evaluating gene expression, and identification of virulence
PT genes
XX

PS Claim 3; Pages 239-240; 333pp; English.
XX

This represents a *S. pneumoniae* putative ATPase involved in membrane functions. The invention provides DNA sequences (AAV65201 to AAV65304) from the *Streptococcus pneumoniae* genome and corresponding protein sequences (AAW80605 to AAW80728). The protein sequences are classified as hypothetical, cell wall biosynthetic, external target, or minimal gene set proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the proteins. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in *S. pneumoniae* and for identifying virulence genes in *S. pneumoniae*. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat *S. pneumoniae* infection. The antibodies can also be used to detect *S. pneumoniae* cells.

The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the *Streptococcus pneumoniae* type 4 strain genomic sequence appearing as AB556454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a *Streptococcus* nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a *Streptococcus pneumoniae* bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to *Streptococcus* bacteria, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences.

Search completed: November 13, 2003, 15:05:01
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 13, 2003, 15:04:11 ; Search time 21 Seconds
(without alignments)
427.138 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVIMDDWPGVDLN.....LDYNEFRDLNHCIVINEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1069	95.8	225	4	US-09-786-240-4
2	772	69.2	218	1	US-08-644-664B-14
3	772	69.2	218	2	US-08-761-277A-14
4	263.5	23.6	200	4	US-09-107-532A-4646
5	238.5	21.4	181	4	US-09-134-001C-3318
6	190	17.0	178	4	US-09-328-352-4965
7	157	14.1	214	4	US-09-252-991A-30612
8	119	10.7	179	4	US-09-107-532A-5030
9	96	8.6	182	4	US-08-920-803A-2
10	96	8.6	182	4	US-08-920-803A-4
11	89	8.0	187	4	US-09-134-001C-4780
12	88.5	7.9	1028	4	US-09-328-352-5749
13	87	7.8	494	3	US-08-993-250-3
14	87	7.8	892	1	US-07-977-434-12
15	87	7.8	892	1	US-08-458-819-12
16	87	7.8	892	5	PCT-US91-07035-12
17	84.5	7.6	207	4	US-09-252-991A-17055
18	84.5	7.6	272	4	US-09-107-532A-5898
19	82	7.3	834	4	US-09-252-991A-31321
20	78.5	7.0	203	4	US-09-134-001C-4797
21	78.5	7.0	415	4	US-09-134-001C-5077
22	78.5	7.0	419	4	US-09-328-352-6451
23	78	7.0	1038	3	US-09-541-782-4
24	78	7.0	1038	4	US-09-723-820-4
25	77	6.9	503	4	US-09-252-991A-32777
26	77	6.9	1169	1	US-08-315-468-4
27	75.5	6.8	1218	4	US-09-589-567-2

28	75	6.7	641	4	US-09-724-623-76	Sequence 76, Appl
29	74.5	6.7	285	3	US-09-327-681-6	Sequence 6, Appl
30	74.5	6.7	1454	4	US-09-328-352-5793	Sequence 5793, Ap
31	74	6.6	420	4	US-09-107-532A-4045	Sequence 4045, Ap
32	73.5	6.6	287	4	US-09-107-532A-4530	Sequence 4530, Ap
33	73.5	6.6	313	4	US-09-134-001C-5621	Sequence 5621, Ap
34	73	6.5	329	4	US-09-107-532A-4092	Sequence 4092, Ap
35	72.5	6.5	375	4	US-09-107-532A-5089	Sequence 5089, Ap
36	72.5	6.5	943	1	US-08-455-970A-10	Sequence 10, Appl
37	72	6.5	396	3	US-09-273-686-2	Sequence 2, Appl
38	71.5	6.4	362	4	US-09-252-991A-31766	Sequence 31766, A
39	71.5	6.4	480	4	US-09-252-991A-28668	Sequence 28668, A
40	71.5	6.4	566	2	US-08-920-095-3	Sequence 3, Appl
41	71.5	6.4	566	5	PCT-US96-05800-3	Sequence 3, Appl
42	71.5	6.4	569	2	US-08-467-822-26	Sequence 26, Appl
43	71.5	6.4	569	3	US-08-432-697-26	Sequence 26, Appl
44	71.5	6.4	569	3	US-08-466-248-26	Sequence 26, Appl
45	71.5	6.4	777	1	US-08-526-964-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-786-240-4
; Sequence 4, Application US/09786240
; Patent No. 6558935
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: HILMAN, Jennifer L.
; APPLICANT: AZIMZAI, Valda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592 PCT
; CURRENT APPLICATION NUMBER: US/09/786,240
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/133,642
; PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6558935 1404963CD1
US-09-786-240-4

Query Match 95.8%; Score 1069; DB 4; Length 225;

Best Local Similarity 98.5%; Pred. No. 1.8e-119;

Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	7	GVWIMDDWPGYDNLNFTY	PQHYGDL	VEYLIP	PHGII	VDRIER	LAKDIM	KDGYSDIM	VLC	66		
Db	14	GVWIMDDWPGYDNLNFTY	PQHYGDL	VEYLIP	PHGII	VDRIER	LAKDIM	KDGYSDIM	VLC	73		
Qy	67	VLKGGYKFCADL	VEHLKNI	SRNSDR	FVSMKV	DFTR	LKSYR	NDQSM	GENQII	IGGGDLSTLA	126	
Db	74	VLKGGYKFCADL	VEHLKNI	SRNSDR	FVSMKV	DFTR	LKSYR	NDQSM	GENQII	IGGGDLSTLA	133	
Qy	127	GKNFLIV	EDVVG	TGRT	TKALLS	NI	EKYP	KNMKV	ASLLV	KTSRSDGFRPDYAGFEI	PHL	186
Db	134	GKNFLIV	EDVVG	TGRT	TKALLS	NI	EKYP	KNMKV	ASLLV	KTSRSDGFRPDYAGFEI	PHL	193
Qy	187	FVVG	YALD	YNE	YFRDL	NH	ICV	INE	HG	212		
Db	194	FVVG	YALD	YNE	YFRDL	NH	ICV	INE	HG	219		

```

RESULT 2
US-08-644-664B-14
; Sequence 14, Application US/08644664B
; Patent No. 5776746
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Gene Amplification Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664B
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane B.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: GENITOPE-00912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-644-664B-14

Query Match 69.2%; Score 772; DB 1; Length 218;
Best Local Similarity 67.9%; Pred. No. 5.3e-84;
Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDPCYDNLNFTYPOHYGDLVYLPHGIIVDRIERLAKDIMKDIGS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MPTRSPSVVISDDEPGYDLDFCIPNHYAEDLEKVFIPHGLIMDRTERLARDVMKMGH 60

QY 61 DIMLVCVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKS YRNDOSMGEMQIIGG 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 HIVALCVLKGKGFADLDYIKALNRNSDRSIPMTVDFIRLKS YCNDOSTGDIKVIIGD 120

QY 121 DLSTLAGKNFLIVEDVVGTRTKALLSNI EKYPKNMKIVASLLVKRTSRSDGFRPDYAG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 DLSTLTGKNVLIVEDIIDTGKTMQTLLSLVKQYSPKQVKVASLLVKRTSRSGYRDFVG 180

QY 181 FEIPLFVVGVALDYNEFRDLNHCIVNEHG 212
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 FEIPDKFVVGVALDYNEFRNLNHCIVSETG 212

RESULT 3
US-08-761-277A-14
; Sequence 14, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP

```

```

; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOPE-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-761-277A-14

Query Match 69.2%; Score 772; DB 2; Length 218;
Best Local Similarity 67.9%; Pred. No. 5.3e-84;
Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDPCYDNLNFTYPOHYGDLVYLPHGIIVDRIERLAKDIMKDIGS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MPTRSPSVVISDDEPGYDLDFCIPNHYAEDLEKVFIPHGLIMDRTERLARDVMKMGH 60

QY 61 DIMLVCVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKS YRNDOSMGEMQIIGG 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 HIVALCVLKGKGFADLDYIKALNRNSDRSIPMTVDFIRLKS YCNDOSTGDIKVIIGD 120

QY 121 DLSTLAGKNFLIVEDVVGTRTKALLSNI EKYPKNMKIVASLLVKRTSRSDGFRPDYAG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 DLSTLTGKNVLIVEDIIDTGKTMQTLLSLVKQYSPKQVKVASLLVKRTSRSGYRDFVG 180

QY 181 FEIPLFVVGVALDYNEFRDLNHCIVNEHG 212
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 FEIPDKFVVGVALDYNEFRNLNHCIVSETG 212

RESULT 4
US-09-107-532A-4646
; Sequence 4646, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>

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Query Match 21.4%; Score 238.5; DB 4; Length 181;
Best Local Similarity 33.5%; Pred. No. 2.2e-20;
Matches 62; Conservative 38; Mismatches 56; Indels 29; Gaps 7;

QY 31 DLEYVLPHGIIVDRIERLAKDIMKDIG-----YSDIWVLCV--LKGGYKFCADLVEHL 82
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Db 6 DLKNVLLS-----EDIQNICKEMGAIITEDYKDRPLVCVGILKGSYMFMDLIKRI 57
:::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 83 KNISRSNDRFVSMMKVDFIRLKSyr-NDOQSMGEHQIICGGDL-STLAGKNFLIVEDVVGTG 140
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 58 D-----THLSIDFMVDSSVHGCTESTGEVQL--XDLGASIEKNKOVLIIEDILETG 106
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 141 RTMKALLSNIEKYKPNMIKVASLLVKRTSRSDGRPDYAGFEIPHLFVVGVALDYNEYFR 200
|||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 107 TTLKSITELQSRKVNSLFIATLLDKPNNRKADIEAKYVGVKKIPDEFVVGYGLDYRELYR 166
|||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 201 DLNHI 205
:|:|
Db 167 NLPIY 171
:|:|

RESULT 6
US-09-328-352-4965
; Sequence 4965, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4965
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4965

Query Match 17.0%; Score 190; DB 4; Length 178;
Best Local Similarity 26.0%; Pred. No. 1.3e-14;
Matches 50; Conservative 44; Mismatches 60; Indels 38; Gaps 6;

QY 35 VLIHGHIIVDRIERLAKDIMKDIGHSD--IMVLCVKGKYKFCADLVEHLKNISNRDRF 92
:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 10 IMISTEEIQAKVKELGEQINSHYANSDELVLIGLRGSVIPFADL---CRTTKPHE-- 64
|||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 93 VSMKVDIFRLKSrYRNDOQSMGEHQIICGGDLST-----LAGKNFLIVEDVVGTG 140
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 65 ----LDPWTVSSY-----GGTTSRDVKILKDLGEGRGDKLVVEDIIDSG 108
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 141 RTMKALLSNIEKYKPNMIKVASLLVKRTSRSDGRPDYAGFEIPHLFVVGVALDYNEYFR 200
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 109 NTLSKVVMELQTRFPNSIQLCTLVSKPSRRRIDLEVLFGEVEDKFIVGYGLDYDQKYR 168
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 201 DLNHICVINEHG 212
:|:|
Db 169 ---HLPFIGEIG 177
:|:|

RESULT 7
US-09-252-991A-30612
; Sequence 30612, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30612
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30612

Query Match
Best Local Similarity 14.1%; Score 157; DB 4; Length 214;
Matches 42; Conservative 36; Mismatches 66; Indels 16; Gaps 4;

QY 46 IERLAKDIMKIDIGSDIMVLCVKGKFCADLVHKLKNIERNSDRFVSMKVDFIRLKS 105
DB 57 IGRVAEAINRDLGETNPVVFVCMNGGLIFSGKLLPLD-----FPLELSYLHATRY 107

QY 106 RNDOSMGEMQIIGGDLTLACKNFIIVDVGTGRTMKALLSNIEKYPKNIKVASLLV 165
DB 108 RNETSGGELFWKAPKPEISFI-DRDVLIIIDDLDEGHTLSAIDFCCKHAGARAVHTAIVLD 166

QY 166 KRTSRSDGRPD-----YAGFEIPHLFVVVGALDYNEYFRD 201
DB 167 KEHERK--ARPDLKASFTGLYCADRYVFGYGM DYKGYWRN 204

RESULT 8
US-09-107-532A-5030
; Sequence 5030, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5030:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...179
; SEQUENCE DESCRIPTION: SEQ ID NO: 5030:
US-09-107-532A-5030

Query Match
Best Local Similarity 10.7%; Score 119; DB 4; Length 179;
Matches 39; Conservative 37; Mismatches 61; Indels 16; Gaps 7;

QY 42 IVDRI-----ERLAKDIM-KDIGSDIMVLCVKGKFCADLVHKLKNIERNSDRFVS 94
DB 6 VVDQVTMKRATRTYIEIERNHSIQDIVLVGIKTRGIYIASRIARLXQLED-----ID 60

QY 95 MKVPFIRLKSRYNDQSMG-ENQIIGGDLs-TLACKNFIIVDVGTGRTMKALLSNIEK 152
DB 61 IPVGELDTILYRDDKKENPEEPHELSSDIPVSLGKVLIDDLVLTGRTIRAAMDAMD 120

QY 153 Y-KNMIVKASLLVKRTSRSDGFRPDYAGFIP 184
DB 121 FGRPKISLA-VLVDGRHRELPIRADYVGKNIP 152

RESULT 9
US-08-920-803A-2
; Sequence 2, Application US/08920803A
; Patent No. 6331410
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin T.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: No. 6331410el pyrR Homolog
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,803A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Q. Todd
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: GM10086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215/994-2252
; TELEFAX: 215/994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-920-803A-2

Query Match
Best Local Similarity 8.6%; Score 96; DB 4; Length 182;
Matches 40; Conservative 36; Mismatches 71; Indels 8; Gaps 6;

QY 33 EYVLPHGIIVDRIERLAKDIMKIDIGSDIMVLCVKGKFCADLVHKLKNIERNSDRF 92
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Db 3 ERIIMDDAAIORTVTRIAHEILEYVKNKGTNDNLLILGKTRGEYLANRIOD-KIHQIEQORI 61
Qy 93 VSMKVDIFRLKSYND-QSMGEMQIIGGGDLST-LAGKNFLIVEDVVGTRTMKALLSNI 150
Db 62 PTGTID---ITYFRDDIEHMSLTTKDAIDITDITDKWIIIDDVLYTGRTVRASLDI 118
Qy 151 -EKYKPNMKIVASLLVKRTSRSDGFRPDYAGFEIP 184
Db 119 LLNARPIKIGLAA-LVDRGHRPELPIRADFVGKNIP 152

RESULT 10
US-08-920-803A-4
; Sequence 4, Application US/08920803A
; Patent No. 6331410
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin T.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: No. 6331410el pyrR Homolog
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/920.803A
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Q. Todd
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: G410086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215/994-2252
; TELEFAX: 215/994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-920-803A-4

Query Match
Best Local Similarity 8.6%; Score 96; DB 4; Length 182;
Matches 40; Conservative 36; Mismatches 71; Indels 8; Gaps 6;

Qy 33 EYVLPHGIIIVDRIERLAKDIMGYSDIMVLCVKGKFCADLVEHLKKNISRNSDRF 92
Db 3 ERIIMDDAAIORTVTRIAHEILEYVKNKGTNDNLLILGKTRGEYLANRIOD-KIHQIEQORI 61
Qy 93 VSMKVDIFRLKSYND-QSMGEMQIIGGGDLST-LAGKNFLIVEDVVGTRTMKALLSNI 150
Db 62 PTGTID---ITYFRDDIEHMSLTTKDAIDITDITDKWIIIDDVLYTGRTVRASLDI 118
Qy 151 -EKYKPNMKIVASLLVKRTSRSDGFRPDYAGFEIP 184
Db 119 LLNARPIKIGLAA-LVDRGHRPELPIRADFVGKNIP 152
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RESULT 11
US-09-134-001C-4780
; Sequence 4780, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC-007
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4780
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4780

Query Match
Best Local Similarity 8.0%; Score 89; DB 4; Length 187;
Matches 41; Conservative 31; Mismatches 31; Indels 18; Gaps 6;

Qy 33 EYVLPHGIIIVDRIERLAKDIMGYSDIMVLCVKGKFCADLVEHLKKNISRNSDR 91
Db 15 ERIILDEAAIORTITRIHAHEILEYVKNKGTDLVLL-----GIKTRGAFLAHRTQDKINSIE 69
Qy 92 FVSMKVDIFRLKSYNDQSMGEMQIIGGGDLST-----LAGKNFLIVEDVVGTRTMKA 145
Db 70 QQLVPTGTIDITHFRDDVD---KVVQADQAYAFDINNVKVVIIIDDVLYTGRTVRA 125
Qy 146 LLSNIEKY-KPNMIKVASLLVKRTSRSDGFRPDYAGFEIP 184
Db 126 SLDAILLHTRPIKIGLAA-LVDRGHRPELPIRADFVGKNIP 164

RESULT 12
US-09-328-352-5749
; Sequence 5749, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5749
; LENGTH: 1028
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5749

Query Match
Best Local Similarity 7.9%; Score 88.5; DB 4; Length 1028;
Matches 34; Conservative 42; Mismatches 61; Indels 25; Gaps 7;

Qy 33 EYVLPHGIIIVDRIERLAKDIMGYSDIMVLCVKGKFCADLVEHLKKNISRNSDRF 92
Db 594 ELDIAP-GVKASKVTNISRDLARSMASVRVVEIPGKPYIGIEV-----PNSARE 644
Qy 93 VSMKVDIFRLKSYNDQSMGEM-----QIIGGGDLSTLAGKNFLIVEDVVGTRTM---KA 145
Db 645 MVRLLIELETFAYDRPSALISMGAKDISGNPVLTDLAKAPHLVAGTTGSGKSVAVNSM 704
Qy 146 LLSNIEKYKPNMIKVASLLVKRTSRSDGFRPDYAGF-EIPIHL 186
Db 705 ILSMLLKYPDQLRL--ILI-----DPKQLELANYNIDPHL 738
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RESULT 13
US-08-993-260-3
; Sequence 3, Application US/08993260
; Patent No. 6031089
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J.
; TITLE OF INVENTION: No. 6031089el Sequences of p56, a Proteins Which
; TITLE OF INVENTION: Affects K-ATP Channels
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Co., Intel. Prop. Law
; ADDRESS: (1920-32-LAW)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,260
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 6092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 833-7914
; TELEFAX: (616) 833-8897
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
;
US-08-993-260-3
Query Match 7.8%; Score 87; DB 3; Length 494;
Best Local Similarity 20.4%; Pred. No. 0.13;
Matches 56; Conservative 38; Mismatches 84; Indels 96; Gaps 13;

Qy 13 DWPGYDNLFTYPOHYGDLBYLIPHGIIVDRIERIAKDIKIDIGYSDIMVLCKGGY 72
Db 124 DW--YLLNLFRLMWHY-----GISFLQMMVVEYVNEKF---MRIYKYQAHGY 166
Qy 73 KFCADLYEHL-----KNISRNS-----DRFVSMKVDFIRLKSRYNDQSM- 111
Db 167 AFSG--VEELYSIGESTFVNMTQSHVAESLLQGVGTORFIDDDVVSALVRASYGQSAAP 224
Qy 112 ---GEMQIIGG-GDLSTLAGNFIIVEDV--VGRGRTKMALLSNIKYKP----- 155
Db 225 AFAGMSIAGAQGSLWSVEGGNKLVCSGLLKLTKANVIAHTVSTVLHSTGKALYQVAY 284
Qy 156 -----NMUKVASLIIVKTRSRD-----GFRP-----D 177
Db 285 ENEGVNSDDFYDVIIVATPLPLDNLSSNNLTTFAGFHPDIDDVQGSFQPTWSLVHGLNNS 344
Qy 178 YAGFEIPLHFLVVGVAL--DYNEYFRDLNHHICVIN 209
Db 345 YFGFPDPLKFLPFANILITDFPSFCTLDNICPVN 378

RESULT 14
US-07-977-434-12

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; Sequence 12, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: WordPerfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cseri
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-07-977-434-12

Query Match      7.8%; Score 87; DB 1; Length 892;
Best Local Similarity 20.7%; Pred. No. 0.33;
Matches 45; Conservative 41; Mismatches 73; Indels 58; Gaps 10;

QY 29 YGDLEYVLPHGIIVDRIERLAKDIMKDI-----GYSDIM 63
DB 212 YNSLENVLKNNILTEKLRRLLEDSKDLQKSIELVELIYVPMDEVKEDEIIRGYNPDK 271
QY 64 VLVKLGKGYKFC-----DLVEHLKN---ISRNSDRFVSMKVDYFIRLKSYNRNDQSMG--- 112
DB 272 LLKVLK-KYFSSIIKELNLOEKEVILVDNEDKLKLAEEIEKYKTFSDTETTSLD 330
QY 113 --EMQIIGGDLSTLAGKNFLIVEDVGTGRMTKALLSNIEKYKPNMKVASLLVKRTS- 169
DB 331 PFEAKLV-GISISTMEGRAYIPVSHFGAKNISKSL---IDKFLKQILQEKDYNIVGQNL 386
QY 170 -----RSDGFRPDYAGFEIPEHL--FVVGVALDYNE 197
DB 387 KFDYEIFKSMGFSPN-----VPHFDTMTIAAYLLNPDE 418

Search completed: November 13, 2003, 15:07:26
Job time : 22 secs

; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
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; FILING DATE: 20-SEP-1990
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; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-819-12

Query Match      7.8%; Score 87; DB 1; Length 892;
Best Local Similarity 20.7%; Pred. No. 0.33;
Matches 45; Conservative 41; Mismatches 73; Indels 58; Gaps 10;

QY 29 YGDLEYVLPHGIIVDRIERLAKDIMKDI-----GYSDIM 63
DB 212 YNSLENVLKNNILTEKLRRLLEDSKDLQKSIELVELIYVPMDEVKEDEIIRGYNPDK 271
QY 64 VLVKLGKGYKFC-----DLVEHLKN---ISRNSDRFVSMKVDYFIRLKSYNRNDQSMG--- 112
DB 272 LLKVLK-KYFSSIIKELNLOEKEVILVDNEDKLKLAEEIEKYKTFSDTETTSLD 330
QY 113 --EMQIIGGDLSTLAGKNFLIVEDVGTGRMTKALLSNIEKYKPNMKVASLLVKRTS- 169
DB 331 PFEAKLV-GISISTMEGRAYIPVSHFGAKNISKSL---IDKFLKQILQEKDYNIVGQNL 386
QY 170 -----RSDGFRPDYAGFEIPEHL--FVVGVALDYNE 197
DB 387 KFDYEIFKSMGFSPN-----VPHFDTMTIAAYLLNPDE 418

RESULT 15
US-08-458-819-12
; Sequence 12, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: WordPerfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,819
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,434
; FILING DATE: 23-FEB-1993
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
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GenCore version 5.1.6
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(without alignments)
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Title: US-09-902-705-2

Perfect score: 1116

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Minimum DB seq length: 0

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

POST-PROCESSING: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW PUB.pcp.*
- 3: /cgn2_6/prodata/2/pubpaa/us06 NEW PUB.pcp.*
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- 6: /cgn2_6/prodata/2/pubpaa/PCTUS PUBCOMB.pcp.*
- 7: /cgn2_6/prodata/2/pubpaa/us08 NEW PUB.pcp.*
- 8: /cgn2_6/prodata/2/pubpaa/us08 PUBCOMB.pcp.*
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- 10: /cgn2_6/prodata/2/pubpaa/us09B PUBCOMB.pcp.*
- 11: /cgn2_6/prodata/2/pubpaa/us09C PUBCOMB.pcp.*
- 12: /cgn2_6/prodata/2/pubpaa/us09 NEW PUB.pcp.*
- 13: /cgn2_6/prodata/2/pubpaa/us10A PUBCOMB.pcp.*
- 14: /cgn2_6/prodata/2/pubpaa/us10B PUBCOMB.pcp.*
- 15: /cgn2_6/prodata/2/pubpaa/us10C PUBCOMB.pcp.*
- 16: /cgn2_6/prodata/2/pubpaa/us10 NEW PUB.pcp.*
- 17: /cgn2_6/prodata/2/pubpaa/us60 NEW PUB.pcp.*
- 18: /cgn2_6/prodata/2/pubpaa/us60 PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			Description	
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1	1116	100.0	212	9	US-09-189-833B-2
2	1116	100.0	212	9	US-09-903-705-2
3	1069	95.8	225	12	US-10-437-631-4
4	786	70.4	218	9	US-09-189-833B-8
5	786	70.4	218	9	US-09-903-705-8
6	779	69.8	218	9	US-09-189-833B-7
7	779	69.8	218	9	US-09-903-705-7
8	772	69.2	218	10	US-09-935-664-14
9	446.5	40.0	231	9	US-09-189-833B-9
10	446.5	40.0	231	9	US-09-903-705-9
11	339	30.4	230	12	US-10-102-143-13
12	251.3	22.9	194	10	US-09-738-626-6465
13	233.5	20.5	186	15	US-10-156-761-12199
14	222.5	19.9	210	9	US-09-189-833B-10
15	222.5	19.9	210	9	US-09-903-705-10

ALIGNMENTS

RESULT 1

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US-09-189-833B-2
; Sequence 2, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-2

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Query Match	100.0%	Score 1116;	DB 9;	Length 212;
Best Local Similarity	100.0%;	Prod. No. 1.3e-115;		
Matches 212;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MATSPGVVIMDDWPGYDLNFTTPOHYYGDEYVLPHGIIIVDRIERLAKDIMKDTIGYS	60
Db	1	MATSPGVVIMDDWPGYDLNFTTPOHYYGDEYVLPHGIIIVDRIERLAKDIMKDTIGYS	60
QY	61	DIWLVCLVKGKGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKSRYNDQSGMGEQIIIGGG	120
Db	61	DIWLVCLVKGKGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKSRYNDQSGMGEQIIIGGG	120
QY	121	DLSTLAGKNFLIIVDDVVGCTGTMTKALLSNIEKYKPNMIKVASLLVKTSTRSDGFRPDYAG	180
Db	121	DLSTLAGKNFLIIVDDVVGCTGTMTKALLSNIEKYKPNMIKVASLLVKTSTRSDGFRPDYAG	180

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; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175923A1 1404963CD1
US-10-427-631-4

Query Match          95.8%; Score 1069; DB 12; Length 225;
Best Local Similarity 98.5%; Pred. No. 2.4e-110;
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDIIGG 66
Db 14 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDIIGG 73
QY 67 VLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMOII 126
Db 74 VLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMOII 133
QY 127 GKNFLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDGFRPDYAG 186
Db 134 GKNVLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDGFRPDYAG 193
QY 187 FVVGVALDYNEYFRDLNHCIVINEHG 212
Db 194 FVVGVALDYNEYFRDLNHCIVINEHG 219

RESULT 4
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138PD1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match          70.4%; Score 786; DB 9; Length 218;
Best Local Similarity 69.3%; Pred. No. 5.8e-79;
Matches 147; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDI 60
Db 1 MATRSPGVVISDDEPGYDLDFCIPNHVYDELEKVFIPHGIVMDTERLARDVMKMG 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMO 120
Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDVFIRLKSYRNDQSMGEMO 120
QY 121 DLSTLAGKNFLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDG 180
Db 121 DLSTLTKGNVLIVEDIIDGKTMQTLVSLVKRNPMMKVASLLVKRTSRSDGFRPDY 180
QY 181 FEIPHLFVVGVALDYNEYFRDLNHCIVINEHG 212
Db 181 FEIPDKFVVGVALDYNEYFRDLNHCIVISG 212

; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175923A1 1404963CD1
US-10-427-631-4

Query Match          95.8%; Score 1069; DB 12; Length 225;
Best Local Similarity 98.5%; Pred. No. 2.4e-110;
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDIIGG 66
Db 14 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDIIGG 73
QY 67 VLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMOII 126
Db 74 VLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMOII 133
QY 127 GKNFLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDGFRPDYAG 186
Db 134 GKNVLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDGFRPDYAG 193
QY 187 FVVGVALDYNEYFRDLNHCIVINEHG 212
Db 194 FVVGVALDYNEYFRDLNHCIVINEHG 219

RESULT 4
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138PD1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match          70.4%; Score 786; DB 9; Length 218;
Best Local Similarity 69.3%; Pred. No. 5.8e-79;
Matches 147; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDI 60
Db 1 MATRSPGVVISDDEPGYDLDFCIPNHVYDELEKVFIPHGIVMDTERLARDVMKMG 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMO 120
Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDVFIRLKSYRNDQSMGEMO 120
QY 121 DLSTLAGKNFLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDG 180
Db 121 DLSTLTKGNVLIVEDIIDGKTMQTLVSLVKRNPMMKVASLLVKRTSRSDGFRPDY 180
QY 181 FEIPHLFVVGVALDYNEYFRDLNHCIVINEHG 212
Db 181 FEIPDKFVVGVALDYNEYFRDLNHCIVISG 212

; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175923A1 1404963CD1
US-10-427-631-4

Query Match          95.8%; Score 1069; DB 12; Length 225;
Best Local Similarity 98.5%; Pred. No. 2.4e-110;
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDIIGG 66
Db 14 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDIIGG 73
QY 67 VLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMOII 126
Db 74 VLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMOII 133
QY 127 GKNFLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDGFRPDYAG 186
Db 134 GKNVLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDGFRPDYAG 193
QY 187 FVVGVALDYNEYFRDLNHCIVINEHG 212
Db 194 FVVGVALDYNEYFRDLNHCIVINEHG 219

RESULT 4
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138PD1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-2

Query Match          100.0%; Score 1116; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.3e-115;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDI 60
Db 1 MATRSPGVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDIMKDI 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMO 120
Db 61 DIMVLVLKGGYKFCADLVEHLKNISRNSDRFVSMKVDVFIRLKSYRNDQSMGEMO 120
QY 121 DLSTLAGKNFLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDG 180
Db 121 DLSTLAGKNFLIVEDVVGTRMTKALLSNIIEKYKPNMIKVASLLVKRTSRSDG 180
QY 181 FEIPHLFVVGVALDYNEYFRDLNHCIVINEHG 212
Db 181 FEIPHLFVVGVALDYNEYFRDLNHCIVINEHG 212

RESULT 3
US-10-427-631-4
; Sequence 4, Application US/10427631
; Publication No. US20030175923A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; LAH, Preeti G.;
; APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592-1 DIV
; CURRENT APPLICATION NUMBER: US/10/427,631
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 09/786,240
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US99/20989
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: US 60/172,220
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/155,248
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/133,642
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 33

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RESULT 5
US-09-902-705-8
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetulus longicaudatus
US-09-902-705-8

Query Match
Best Local Similarity 70.4%; Score 786; DB 9; Length 218;
Matches 147; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNFTYPOHYGDLLEYVLPHGIIVDRTERLAKDIMKDIGYS 60
Db 1 MATRSPGVISDDEFGYDLDFCIPNHVYEDLEKVFIPHGVMIDRTERLARDVMKEMGGH 60

QY 61 DIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKS YRNDOSMGEMQIIGGG 120
Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKS YCNDQSTGDIKVIIGD 120

QY 121 DLSTLAGKNFLIVEDVVGTRTKMALLSNI EKYPKNMIKVASLLVKRTS RSDGFRPDYAG 180
Db 121 DLSTLTGKNVLIVEDIIDTGMTQTL SLVRQYNPNMKVVASLLVKRTSPRSVGYKPDFVG 180

QY 181 FEIPHLFVVGVALDYNE YFRDLNHCIVINEHG 212
Db 181 FEIPDKFVVGYALDYNE YFRDLNHCIVISETG 212

RESULT 6
US-09-189-833B-7
; Sequence 7, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-7

Query Match
Best Local Similarity 69.8%; Score 779; DB 9; Length 218;
Matches 145; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNFTYPOHYGDLLEYVLPHGIIVDRTERLAKDIMKDIGYS 60
Db 1 MATRSPGVISDDEFGYDLDFCIPNHVYEDLEKVFIPHGVMIDRTERLARDVMKEMGGH 60

QY 61 DIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKS YRNDOSMGEMQIIGGG 120
Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKS YCNDQSTGDIKVIIGD 120

QY 121 DLSTLAGKNFLIVEDVVGTRTKMALLSNI EKYPKNMIKVASLLVKRTS RSDGFRPDYAG 180
Db 121 DLSTLTGKNVLIVEDIIDTGMTQTL SLVRQYNPNMKVVASLLVKRTSPRSVGYKPDFVG 180

QY 181 FEIPHLFVVGVALDYNE YFRDLNHCIVINEHG 212
Db 181 FEIPDKFVVGYALDYNE YFRDLNHCIVISETG 212

RESULT 7
US-09-902-705-7
; Sequence 7, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-7

Query Match
Best Local Similarity 69.8%; Score 779; DB 9; Length 218;
Matches 145; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNFTYPOHYGDLLEYVLPHGIIVDRTERLAKDIMKDIGYS 60
Db 1 MATRSPGVISDDEFGYDLDFCIPNHVYEDLEKVFIPHGVMIDRTERLARDVMKEMGGH 60

QY 61 DIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKS YRNDOSMGEMQIIGGG 120
Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKS YCNDQSTGDIKVIIGD 120

QY 121 DLSTLAGKNFLIVEDVVGTRTKMALLSNI EKYPKNMIKVASLLVKRTS RSDGFRPDYAG 180
Db 121 DLSTLTGKNVLIVEDIIDTGMTQTL SLVRQYNPNMKVVASLLVKRTSPRSVGYKPDFVG 180

QY 181 FEIPHLFVVGVALDYNE YFRDLNHCIVINEHG 212
Db 181 FEIPDKFVVGYALDYNE YFRDLNHCIVISETG 212

RESULT 8
US-09-925-664-14
; Sequence 14, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
; APPLICANT: Denney, Jr., Dan W.
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
; FILE REFERENCE: GENITOPE-06499
; CURRENT APPLICATION NUMBER: US/09/925,664
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/370,453
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 08/644,664
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/761,277
; PRIOR FILING DATE: 1996-12-06
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; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-664-14

Query Match      69.2%; Score 772; DB 10; Length 218;
Best Local Similarity 67.9%; Pred. No. 2.1e-77;
Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVVIMDDWPGYDLNLFYTPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDIGYS 60
DB 1 MPTRSPSVVISDEPGYDLDDFCIHNHVAEDLEKVFPHGLIMDRTERLARDVWKMGGH 60

QY 61 DIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVD FIRLKS YRNDQSMGEMOIIIGG 120
DB 61 HIVALCVLKGKFFADLLDYIKALNRNSDRSIPMTVDFIRLKS YCNDQSTGDIKVIIGD 120

QY 121 DLSTLAGKNFLIVDVGTGRMTKALLSNI EYKPNMIKVASLLVKRTSRSDGPRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIIDTGKTMQTLISLVKQSPRMVKVASLLVKRTSRSGVGRPDFVG 180

QY 181 FEIPLHFLVVGVALDYNEYFRDLNHLHCIVINEHG 212
DB 181 FEIPDKFVGVALDYNEYFRNLNHLVCVSETG 212

RESULT 9
US-09-189-833B-9
; Sequence 9, Application US/09189833B
; Patent No. US20020085393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-189-833B-9

Query Match      40.0%; Score 446.5; DB 9; Length 231;
Best Local Similarity 42.7%; Pred. No. 3e-41;
Matches 93; Conservative 41; Mismatches 73; Indels 11; Gaps 3;

QY 5 SPGV-----VIMDDWPGYDLNLFYTPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDI 57
DB 6 NPGAGENAFDPVFVKDDGDDYDLDSFMI PAHYKKYLT KVLVPNGVKNRIEKLAYDIKKVY 65

QY 58 GYSIDIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVD--DFIRLKS YRNDQSMGEM 114
DB 66 NNEEFHILCLLKSGRGFFTALLKHLSRHNYS AVEMSKPLFGEHVYVRKSYCNDQSTGTL 125

QY 115 QIIGGGDLSTLAGKNFLIVDVGTGRMTKALLSNI EYKPNMIKVASLLVKRTSRSDGF 174
DB 126 EIV-SEDLSC LKGGHVLIVEDIIDTGKTLVKFCEYLKKEIKTVAIACLFIKRTPLWNGF 184

QY 175 RPDYAGFEIPLHFLVVGVALDYNEYFRDLNHLHCIVINEHG 212
DB 185 KADVFVGFSIPDHFVVGYSLDYNEIFRDLDHCCLVNDEG 222

RESULT 11
US-10-102-143-13
; Sequence 13, Application US/10102143
; Publication No. US20030185851A1
; GENERAL INFORMATION:
; APPLICANT: Soldati, Dominique
; APPLICANT: Meissner, Markus
; TITLE OF INVENTION: TET transactivator system
; FILE REFERENCE: 04630/016001
; CURRENT APPLICATION NUMBER: US/10/102,143
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pTetO7SagI-HXGPRT
US-10-102-143-13

Query Match      30.4%; Score 339; DB 12; Length 230;
Best Local Similarity 34.4%; Pred. No. 2.5e-29;
Matches 67; Conservative 50; Mismatches 76; Indels 2; Gaps 2;

QY 17 YDLNLFYTPQHYGGDLEYVLPHGIIVDRIERLAKDIMKOIGYSIDIMVLVLKGGYKFC 76
DB 28 YNADDFLVPPECKPYIDKILLPGGLVKDVRVEKLAYDIHRTYFGBELHICILKSGRGFFN 87

QY 77 DLVEHLKNI SRNSDRFVSMKVD-FIRLKS YRNDQSMGEMQIIGGGDLSTLAGKNFLIVED 135

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OM protein - protein search, using sw model

Run on: November 13, 2003, 15:03:26 ; Search time 20 Seconds
(without alignments)
1019.388 Million cell updates/sec

Title: US-09-902-705-2
Perfect score: 1116
Sequence: 1 MATRSPGVIMDDWPGYDLN.....LDYNEFRDLNHCIVINEHG 212
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	786	70.4	218	2 S43043	hypoxanthine (guan
2	783	70.2	214	2 I49758	hypoxanthine phosp
3	779	69.8	218	1 RTHUG	hypoxanthine phosp
4	779	69.8	218	2 S21474	hypoxanthine phosp
5	777	69.6	218	1 RTMSG	hypoxanthine phosp
6	776	69.5	218	1 RTHYG	hypoxanthine phosp
7	768	68.8	218	2 I51842	hypoxanthine phosp
8	768	68.8	218	2 S18140	hypoxanthine phosp
9	498.5	44.7	285	2 S09614	hypoxanthine phosp
10	485	43.5	284	2 S04278	hypoxanthine phosp
11	447.5	40.1	231	2 S06601	hypoxanthine phosp
12	446.5	40.0	231	2 S06315	hypoxanthine phosp
13	445.5	39.9	231	2 JN0085	hypoxanthine phosp
14	265.5	23.8	180	2 S66098	hypoxanthine phosp
15	265.5	23.8	180	2 G86814	hypothetical prote
16	261	23.4	183	2 S30100	hypoxanthine phosp
17	261	23.4	183	2 D86627	hypothetical prote
18	257.5	23.1	178	2 H97293	hypoxanthine-guani
19	255	22.8	178	2 A70349	hypoxanthine-guani
20	254.5	22.8	648	2 AD1464	fusion protein, N-
21	250.5	22.4	648	2 AD1102	hypoxanthine-guani
22	247.5	22.2	180	2 D95001	hypoxanthine-guani
23	247.5	22.2	180	2 C97873	hypoxanthine phosp
24	244.5	21.9	175	2 T43487	hypoxanthine phosp
25	239.5	21.5	179	2 C69817	hypothetical prote
26	235.5	21.1	187	2 T36331	probable hypoxanth
27	232.5	20.8	179	2 D83660	hypoxanthine-guani
28	229	20.5	171	2 H72405	hypoxanthine phosp
29	227.5	20.4	216	2 A70561	probable hpt prote

30	223.5	20.0	213	2 F86935	probable hypoxanth
31	222.5	19.9	210	2 S41631	hypoxanthine phosp
32	221	19.8	177	2 E82306	hypoxanthine phosp
33	218	19.5	176	2 S10993	hypoxanthine phosp
34	216.5	19.4	182	2 A90645	hypoxanthine phosp
35	216.5	19.4	182	2 A85496	hypoxanthine phosp
36	216.5	19.4	182	2 S45202	hypoxanthine phosp
37	209	18.7	182	2 S19720	hypoxanthine phosp
38	208.5	18.4	176	2 A75404	hypoxanthine-guani
39	205	18.4	180	2 AB3000	hypoxanthine phosp
40	205	18.4	180	2 G98283	hypoxanthine phosp
41	200	17.9	206	2 C82934	hypoxanthine-guani
42	198.5	17.8	178	2 AB0414	hypoxanthine phosp
43	197.5	17.7	178	2 AH0523	hypoxanthine phosp
44	197	17.7	193	2 G90580	hypothetical prote
45	189	16.9	179	2 D64168	hypoxanthine phosp

ALIGNMENTS

RESULT 1

S43043
hypoxanthine (guanine) phosphoribosyltransferase - long-tailed hamster
C;Species: Cricetus longicaudatus (long-tailed hamster)
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C;Accession: S43043
R;Wei, S.J.C.; Chang, R.L.; Bhachech, N.; Cui, X.X.; Merkier, K.A.; Wong, C.Q.; Hennig, Cancer Res. 53, 3294-3301, 1993
A;Title: Dose-dependent differences in the profile of mutations induced by (+)-7R,8S-di-horibosyltransferase gene in chinese hamster V-79 cells.
A;Reference number: S43043; MUID:9333862; PMID:8324741
A;Accession: S43043
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-218 <WEI>
A;Cross-references: EMBL:X59652; NID:g461343; PIDN:CAA42198.1; PID:g461344
C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match	70.4%	Score 786;	DB 2;	Length 218;
Best Local Similarity	69.3%;	Pred. No. 3.1e-59;		
Matches 147;	Conservative 30;	Mismatches 35;	Indels 0;	Gaps 0;
Qy	1	MATRSPGVIMDDWPGYDLNLFYQHYGDLVLPHPGIIIVDRTERLAKDIMKDI	GYS 60	
Db	1	MATRSPSVISDDEPGYDLDFCIPNHYEDELKVFIPHPGVIIMDRTERLARDVNKMGGH	60	
Qy	61	DIIVLCVLKGGYKFCADLVEHLKNISSNSDRFVSMKYVDFIRLKSRYNDQSGEMQII	GGG 120	
Db	61	HIVALCVLKGGYKFFADLDYIRALNNSDRSPMTVDFIRLKSRYNDQSGTDIKVIGGD	120	
Qy	121	DLSTLAGKNFLIVEDVVGTRTKALLSNIETKYPNMIKVASLLVKTSSRSDGFRPDYAG	180	
Db	121	DLSTLTGKNVLIVEDIIDGTQTLQTLVLRKYNPKMKVAVSLVLRKTSRSGVRPDEVG	180	
Qy	181	FEIPLFPVGYALDYNFYFDLNHCIVINEHG	212	
Db	181	FEIPDKFVGYALDYNFYFDLNHCIVISETG	212	

RESULT 2

I49758
hypoxanthine phosphoribosyltransferase (BC 2.4.2.8) - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: I49758
R;Johnson, G.G.; Kronert, W.A.; Bernstein, S.I.; Smith, K.D. J. Biol. Chem. 263, 9079-9082, 1988
A;Title: Altered turnover of allelic variants of hypoxanthine phosphoribosyltransferase
A;Reference number: I49758; MUID:88243783; PMID:3379061
A;Accession: I49758
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: mRNA

Db 1 MATRSPGVVISDDEPGYDLDFCIPNHVYAEADLERVFIPLHGLIMDRTERLARDVMKEMGGH 60
 QY 61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDPIRLKSYRNDQSMGEMQIIGG 120
 Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGD 120
 QY 121 DLSTLAGKNFLIVEDVVGTRTKALLSNIKYKPMIKVASLLVKRTSRSDGFRPDYAG 180
 Db 121 DLSTLTGKNVLIVEDIIDTGKTMQTLISLVQRNPKWVKVASLLVKRTSRSGYKPDFVFG 180
 QY 181 FEIPLHFLVGVGYALDYNFRDLNHCIVNEHG 212
 Db 181 FEIPDKFVVGVALDYNFRDLNHCIVSETG 212

RESULT 4

S21474

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - long-tailed hamster
 N:Alternate names: hypoxanthine guanine phosphoribosyltransferase
 C:Species: Cricetulus longicaudatus (long-tailed hamster)
 C:Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 18-Jun-1999
 C:Accession: S21474
 R:Rossiter, F.; Muzny, M.; Caskey, T.; Fox, M.
 A:Description: A Chinese hamster HPRT point mutation reverts to the wild-type sequence.
 A:Reference number: S21474
 A:Accession: S21474
 A:Molecule type: mRNA
 A:Residues: 1-218 <ROS>
 A:Cross-references: EMBL:X17656; NID:g49514; PIDN:CAA35648.1; PID:g49515
 C:Superfamily: hypoxanthine phosphoribosyltransferase
 C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 69.8%; Score 779; DB 2; Length 218;
 Best Local Similarity 68.9%; Pred. No. 1.2e-58;
 Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNLTYPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDIGYS 60
 Db 1 MATRSPSVVISDDEPGYDLDFCIPNHVYAEADLERVFIPLHGLIMDRTERLARDVMKEMGGH 60
 QY 61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDPIRLKSYRNDQSMGEMQIIGG 120
 Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGD 120
 QY 121 DLSTLAGKNFLIVEDVVGTRTKALLSNIKYKPMIKVASLLVKRTSRSDGFRPDYAG 180
 Db 121 DLSTLTGKNVLIVEDIIDTGKTMQTLISLVQRNPKWVKVASLLVKRTSRSGYKPDFVFG 180
 QY 181 FEIPLHFLVGVGYALDYNFRDLNHCIVNEHG 212
 Db 181 FEIPDKFVVGVALDYNFRDLNHCIVSETG 212

RESULT 5

RTMSG

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - mouse
 N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1989 #sequence revision 09-Aug-1997 #text_change 11-Jun-1999
 C:Accession: I49756; A26218; A00579
 R:Melton, D.W.; Konecki, D.S.; Brennan, J.; Caskey, C.T.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2147-2151, 1984
 A:Title: Structure, expression, and mutation of the hypoxanthine phosphoribosyltransferase
 A:Reference number: I49756; MUID:84193967; PMID:6326107
 A:Accession: I49756
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-218 <RES>
 A:Cross-references: GB:K01515; NID:g193994; PIDN:AAA96271.1; PID:g387206
 R:Konecki, D.S.; Brennan, J.; Fuscoe, J.C.; Caskey, C.T.; Chinault, A.C.
 Nucleic Acids Res. 10, 6763-6775, 1982

A:Title: Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hams
 A:Reference number: A93446; MUID:83090437; PMID:6294614
 A:Accession: A26218
 A:Molecule type: mRNA
 A:Residues: 2-200, 'N', 202-218 <KON>
 A:Cross-references: GB:J00423; NID:g193984; PIDN:AAA96232.1; PID:g309315
 A:Note: initiator Met not shown
 A:Note: this variant protein has enzymatic activity and its sequence is expected to be
 ine having no enzymatic activity
 C:Genetics:
 A:Introns: 9/3; 45/2; 106/3; 128/3; 134/3; 162/2; 178/1; 203/3
 C:Superfamily: hypoxanthine phosphoribosyltransferase
 C:Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 69.6%; Score 777; DB 1; Length 218;
 Best Local Similarity 68.4%; Pred. No. 1.8e-58;
 Matches 145; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNLTYPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDIGYS 60
 Db 1 MPTRSPSVVISDDEPGYDLDFCIPNHVYAEADLERVFIPLHGLIMDRTERLARDVMKEMGGH 60
 QY 61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDPIRLKSYRNDQSMGEMQIIGG 120
 Db 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGD 120
 QY 121 DLSTLAGKNFLIVEDVVGTRTKALLSNIKYKPMIKVASLLVKRTSRSDGFRPDYAG 180
 Db 121 DLSTLTGKNVLIVEDIIDTGKTMQTLISLVQRNPKWVKVASLLVKRTSRSGYKPDFVFG 180
 QY 181 FEIPLHFLVGVGYALDYNFRDLNHCIVNEHG 212
 Db 181 FEIPDKFVVGVALDYNFRDLNHCIVSETG 212

RESULT 6

RTHYG

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - Chinese hamster
 N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase
 C:Species: Cricetulus griseus (Chinese hamster)
 C:Date: 31-Dec-1989 #sequence revision 12-Apr-1996 #text_change 01-Dec-2000
 C:Accession: S14402; A26219; I58003; A00579
 R:Rossiter, B.J.F.; Fuscoe, J.C.; Muzny, D.M.; Fox, M.; Caskey, C.T.
 Genomics 9, 247-256, 1991
 A:Title: The Chinese hamster HPRT gene: restriction map, sequence analysis, and multipl
 A:Reference number: S14402; MUID:91169526; PMID:2004774
 A:Accession: S14402
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-218 <ROS>
 A:Cross-references: EMBL:X53073; NID:g49505; PIDN:CAA37247.1; PID:g817936
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1990
 R:Konecki, D.S.; Brennan, J.; Fuscoe, J.C.; Caskey, C.T.; Chinault, A.C.
 Nucleic Acids Res. 10, 6763-6775, 1982
 A:Title: Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hams
 A:Reference number: A93446; MUID:83090437; PMID:6294614
 A:Accession: A26219
 A:Molecule type: mRNA
 A:Residues: 2-218 <KON>
 A:Cross-references: GB:J00060; NID:g191112; PIDN:AAA36990.1; PID:g304515
 A:Note: initiator Met not shown
 A:Note: this variant protein has enzymatic activity and its sequence is expected to be
 ine having no enzymatic activity
 R:Fuscoe, J.C.; Zimmerman, L.J.; Pekete, A.; Setzer, R.W.; Rossiter, B.J.
 Mutat. Res. 269, 171-183, 1992
 A:Title: Analysis of X-ray-induced HPRT mutations in CHO cells: insertion and deletions
 A:Reference number: I58003; MUID:93024555; PMID:1383700
 A:Accession: I58003
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 32-44 <RES>
 A:Cross-references: GB:S46270; NID:g257049
 C:Genetics:

A;Gene: hprt

A;Introns: 9/3; 45/2; 106/3; 128/3; 134/3; 162/2; 178/1; 203/3

C;Superfamily: hypoxanthine phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 69.5%; Score 776; DB 1; Length 218;
Best Local Similarity 68.9%; Pred. No. 21e-58;
Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDPFGYDLNLFTYPOHYGDLLEYVLIIPHGIIVDRIERIAKDIMKDIGYS 60
DB 1 MATRSPSVVVISDDSPFGYDLDFCIPNHVVEDELEKVFIPHGVIIMDRTERLARDVMKEMGGH 60
QY 61 DIMVLCVLKGGYKFCADLVEHLKNISRNDRFVSMKVDFFIRLKSYNRDSQSGEMOIIIGGG 120
DB 61 HIVALCVLKGKYKFFADLDLYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGD 120
QY 121 DLSTLAGKNFLIVDDVGTGRTKALLSNIKEYKPNMIKVASLLVKRTSRSDGPRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIITGKTMTQTLISLVKRYNLKWKVASLLVKRTSRSGVGRPDFVG 180
QY 181 FEIPLHFLVGVGALDYNFYERDLNHCIVNEHG 212
DB 181 FEIPDKFVGVGALDYNFYERDLNHCIVSETG 212

RESULT 7

I51842

hypoxanthine phosphoribosyltransferase - rat

C;Species: Rattus sp. (rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 18-Jun-1999

C;Accession: I51842

R;Chiaverotti, T.A.; Battula, N.; Monnat, R.J.

A;Title: Rat hypoxanthine phosphoribosyltransferase cDNA cloning and sequence analysis.

A;Reference number: I51842; MUID:92142869; PMID:1781355

A;Accession: I51842

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: mRNA

A;Residues: 1-218 <RES>

A;Cross-references: GB:S79292; NID:g244375; PIDN:AAB21288.1; PID:g244376

C;Genetics:

A;Gene: hprt

C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 68.8%; Score 768; DB 2; Length 218;
Best Local Similarity 67.5%; Pred. No. 1e-57;
Matches 143; Conservative 33; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDPFGYDLNLFTYPOHYGDLLEYVLIIPHGIIVDRIERIAKDIMKDIGYS 60
DB 1 MSTLSPSVVVISDDSPFGYDLDFCIPNHVAEDELKVFIPHGVIIMDRTERLARDVMKEMGGH 60
QY 61 DIMVLCVLKGGYKFCADLVEHLKNISRNDRFVSMKVDFFIRLKSYNRDSQSGEMOIIIGGG 120
DB 61 HIVALCVLKGKYKFFADLDLYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGD 120
QY 121 DLSTLAGKNFLIVDDVGTGRTKALLSNIKEYKPNMIKVASLLVKRTSRSDGPRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIITGKTMTQTLISLVKQYSPQMKVASLLVKRTSRSGVGRPDFVG 180
QY 181 FEIPLHFLVGVGALDYNFYERDLNHCIVNEHG 212
DB 181 FEIPDKFVGVGALDYNFYERDLNHCIVSETG 212

RESULT 8

S18140

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - rat

N;Alternate names: hypoxanthine-guanine phosphoribosyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999

C;Accession: S18140; I54169; I58008

R.Jansen, J.; Vrieling, H.; van Zeeland, A.; Mohn, G.
submitted to the EMBL Data Library, August 1991
A:Description: The gene encoding hypoxanthine-guanine phosphoribosyltransferase as targ
A:Reference number: S18140
A:Accession: S18140
A:Molecule type: mRNA
A:Residues: 1-218 <OAN>
A:Cross-references: EMBL:X62085; NID:G56373; PIDN:CAA43987.1; PID:G56374
R:Chiaverotti, T.A.; Battula, N.; Monnat, R.J.
Genomics 11, 1158-1160, 1991
A:Title: Rat hypoxanthine phosphoribosyltransferase cDNA cloning and sequence analysis.
A:Reference number: I54169; MUID:92147115; PMID:1783384
A:Accession: I54169
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-218 <RES>
A:Cross-references: GB:M36383; NID:G204658; PIDN:AAA41350.1; PID:G204659
R:Mittelstaedt, R.A.; Heflich, R.H.
Mutat. Res. 311, 139-148, 1994
A:Title: Analysis of in vivo mutation in exon 8 of the rat hprt gene.
A:Reference number: I58008; MUID:95059140; PMID:7526167
A:Accession: I58008
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 163-203 <RE2>
A:Cross-references: EMBL:U06049; NID:G600482; PIDN:AAA56887.1; PID:G452580
C:Genetics:
A:Gene: hprt
A:Introns: 178/1
C:Superfamily: hypoxanthine phosphoribosyltransferase
C:Keywords: Glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 68.8%; Score 768; DB 2; Length 218;
Best Local Similarity 67.5%; Pred. No.1e-57;
Matches 143; Conservative 33; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATRSPGVIMDMPGYDLNLFYPOHYGDELYVLPHGIIIVDRIERLAKDIMKDIGYS 60
Db 1 MSTLSPSWISDDPEGYDLDFCIPNHYAEDLEKVPFPHGLINMDRTERLARDVNMKGWH 60
Qy 61 DIWVLVLGGYKFCADLVEHLKINSPNDRFVSMKVDFIRLKSYNDSQSGEMQIIGG 120
Db 61 HIVALVLGGYKFFADLDIYKALNNSDRSPMTVDFIRLKSYNDSQSGDKIVIGD 120
Qy 121 DLSTLAGKPLIIVEDVVGVTGRTMKALLSNIEKPKNMKVASLLVKRTSRSDGFRPDYAG 180
Db 121 DLSTLTKGNLIVEDIIDGKTMTLLSVKQSPKMKVASLLVKRTSRSGYRDFDVG 180
Qy 181 FEIPHLFVVGVALDYNEYFRDLNHICVINEHG 212
Db 181 FEIPDRFVVGVALDYNEHFRDLNHVCVISEG 212

RESULT 9
S09614
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni.)
N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase
C:Species: Schistosoma mansoni
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 28-Apr-1993
C:Accession: S09614
R:Craig III, S.P.; Muralidhar, M.G.; McKerrow, J.H.; Wang, C.C.
Nucleic Acids Res. 17, 1635-1647, 1989
A:Title: Evidence for a class of very small introns in the gene for hypoxanthine-guanin-
A:Reference number: S09614; MUID:89160320; PMID:2701934
A:Accession: S09614
A:Molecule type: DNA
A:Residues: 1-285 <CRA>
A:Cross-references: EMBL:X13531
A:Note: the authors did not translate the codons for residues 1-54
C:Genetics:
A:Introns: 66/3; 102/3; 166/3; 188/3; 221/3; 238/1; 263/3
C:Superfamily: hypoxanthine phosphoribosyltransferase
C:Keywords: Glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 44.7%; Score 498.5; DB 2; Length 285;
Best Local Similarity 48.6%; Pred. No. 9e-35;
Matches 101; Conservative 40; Mismatches 64; Indels 3; Gaps 1;

QY 8 VVIMDDPFGVDLNLFTYPQHYYGDLVYLPHGLIIVDRIERLAKDIM---KDICYSDIMV 64
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 65 VVIEDSRGFPTFECTSPRYDECLDVLLIPNGMIKORLEKMSMDIVIDYVEACNATSI TL 124
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 65 LCVILKGKYFCADLVEHLKNIISNRSDRFVSMKKVFIRLKSYRNDQSNGEMQIIIGGGDLS T 124
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 125 MCVLKGGFKFLADLV DGLERTVARGIVLPMSVEFVRVKSVYVNDVSIHEPIITGLGDPS E 184
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 125 LAGKNFLIVEDVGTRGTMTKALLSNIEKKYNPMIKVASLLVKPTRSDGRPDYAGFEIP 184
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 185 YKDNVLVVEDIIDTGTTITKLISHLSLTSTSKVKASLLVKRTSPRNDYRPDVFVGFEVP 244
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 185 HLFVVGVGYALDYNEFRDLNHICVINEHG 212
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 245 NRVVGVGYALDYNDNFRLHHCVINEVG 272
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 10
S04278
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni)
N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase
C:Species: Schistosoma mansoni
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
R:Craig, S.P.; Muralidhar, M.G.; McKerrow, J.H.; Wang, C.C.
submitted to the EMBL Data Library, November 1988
A:Reference number: S04278
A:Accession: S04278
A:Molecule type: DNA
A:Residues: 1-284 <RA>
A:Cross-references: EMBL:X13531; NID:g10181; PIDN:CAA31885.1; PID:g1197381
R:Craig III, S.P.; McKerrow, J.H.; Newport, G.R.; Wang, C.C.
Nucleic Acids Res. 16, 7087-7101, 1988
A:Title: Analysis of cDNA encoding the hypoxanthine-guanine phosphoribosyltransferase (H
A:Reference number: S01201; MUID:88030331; PMID:3136439
A:Accession: S01201
A:Molecule type: mRNA
A:Residues: 1-231 <CRA2>
A:Cross-references: EMBL:X07883
C:Genetics:
A:Introns: 66/3; 102/3; 188/3; 221/3; 237/3; 262/3
C:Superfamily: hypoxanthine phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 43.5%; Score 485; DB 2; Length 284;
Best Local Similarity 48.6%; Pred. No. 1.2e-33;
Matches 101; Conservative 39; Mismatches 64; Indels 4; Gaps 2;

QY 8 VVIMDDPFGVDLNLFTYPQHYYGDLVYLPHGLIIVDRIERLAKDIM---KDICYSDIMV 64
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 65 VVIEDSRGFPTFECTSPRYDECLDVLLIPNGMIKORLEKMSMDIVIDYVEACNATSI TL 124
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 65 LCVILKGKYFCADLVEHLKNIISNRSDRFVSMKKVDFIRLKSYRNDQSNGEMQIIIGGGDLS T 124
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 125 MCVLKGGFKFLADLV DGLERTVARGIVLPMSVEFVRVKSVYVNDVSIHEPIITGLGDPS E 184
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 125 LAGKNFLIVEDVGTRGTMTKALLSNIEKKYNPMIKVASLLVKPTRSDGRPDYAGFEIP 184
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 185 YKDNVLVVEDIIDTGTTITKLISHLSLTSTSKVKASLLVKRTSPRNDYRPDVFVGFEVP 243
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 185 HLFVVGVGYALDYNEFRDLNHICVINEHG 212
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 244 NRVVGVGYALDYNDNFRLHHCVINEVG 271
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 11
S06601
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - malaria parasite (Plasmodium falci)

N|Alternate names: hypoxanthine-guanine phosphoribosyltransferase
C|Species: Plasmodium falciparum
C|Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000
C|Accession: S06601
R|Vasanthakumar, G.; Davis Jr., R.L.; Sullivan, M.A.; Donahue, J.P.
Nucleic Acids Res. 17, 8382, 1989
A|Title: Nucleotide sequence of cDNA clone for hypoxanthine-guanine phosphoribosyltransf
A|Reference number: S06601; MUID:90045974; PMID:2682528
A|Accession: S06601
A|Status: translation not shown
A|Molecule type: mRNA
A|Residues: 1-231 <VAS>
A|Cross-references: EMBL:X16279; NID:g9913; PIDN:CAA34355.1; PID:g9914
C|Superfamily: hypoxanthine phosphoribosyltransferase
C|Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 40.1%; Score 447.5; DB 2; Length 231;
Best Local Similarity 42.7%; Pred. No. 1.4e-30;
Matches 93; Conservative 41; Mismatches 73; Indels 11; Gaps 3;

Qy 5 SPGV-----VMDDWPGVDNLFTYPQHYGDLVLPHGIIIVDRIERLAKDIMKDI 57
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
6 NPGAGENAFDPFVNDDGGYDLSDFMIPAHYKKYLTKVLVPNGVIKNRIEKLAYDIKKVY 65

Qy 58 GYSIMVLCVLKGKYKFCADLVHLEKNISNRSDRFVSMKV---DFIRLKSYRNDSQMGE 114
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
66 NNEEFHILCLLKGSGGFETALLKHLSRHNYSAVETSKPLFGHEHYVRVKSCYNDQSTGTL 125

Qy 115 QIIGGGDLSTLAGNKFLIVEDVVGTGRMTKALLSNIKEYKPNNIKVASLLVKRTSRSDGF 174
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
126 EIV-SEDSLCKGHXHLVIDEIIDTOKTLVKFCEYLKKFEIKTVAIACLFIKRTPLNWGF 184

Qy 175 RPDYAGFEIPHFWVGVALDYNEYFRDLNHICVINEHG 212
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
185 KADPVGSIPDHFFVVGSLDYNEIFRDLDHCCLVNDSEG 222

RESULT 12
S06315
hypoxanthine phosphoribosyltransferase (BC 2.4.2.8) - malaria parasite (Plasmodium falci
C|Species: Plasmodium falciparum
C|Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jun-2000
C|Accession: S06315
R|King, A.; Melton, D.W.
Nucleic Acids Res. 15, 10469-10481, 1987
A|Title: Characterisation of cDNA clones for hypoxanthine-guanine phosphoribosyltransfe
A|Reference number: S06315; MUID:98096579; PMID:3320967
A|Accession: S06315
A|Status: not compared with conceptual translation
A|Molecule type: mRNA
A|Residues: 1-231 <KIN>
A|Cross-references: GB:X00519; NID:g9901; PIDN:CAAG68573.1; PID:g9902
C|Superfamily: hypoxanthine phosphoribosyltransferase
C|Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 40.0%; Score 446.5; DB 2; Length 231;
Best Local Similarity 42.7%; Pred. No. 1.8e-30;
Matches 93; Conservative 41; Mismatches 73; Indels 11; Gaps 3;

Qy 5 SPGV-----VMDDWPGVDNLFTYPQHYGDLVLPHGIIIVDRIERLAKDIMKDI 57
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
6 NPGAGENAFDPFVFVKDDGGYDLSDFMIPAHYKKYLTKVLVPNGVIKNRIEKLAYDIKKVY 65

Qy 58 GYSIMVLCVLKGKYKFCADLVHLEKNISNRSDRFVSMKV---DFIRLKSYRNDSQMGE 114
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
66 NNEEFHILCLLKGSGGFETALLKHLSRHNYSAVENSKPLFGHEYVRVKSCYNDQSTGTL 125

Qy 115 QIIGGGDLSTLAGNKFLIVEDVVGTGRMTKALLSNTKEYKPNNIKVASLLVKRTSRSDGF 174
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
126 EIV-SEDSLCKGHXHLVIDEIIDTOKTLVKFCEYLKKFEIKTVAIACLFIKRTPLNWGF 184

Qy 175 RPDYAGFEIPHFWVGVALDYNEYFRDLNHICVINEHG 212
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 185 KADFGVGSIPDHFVVGYSLDYNEIFRDLDHCLVNDG 222

RESULT 13

JN0085

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - malaria parasite (Plasmodium falciparum)

N:Alternate names: 26k trophozoite antigen IC11-53; guanine phosphoribosyltransferase; h

C:Species: Plasmodium falciparum

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jun-2000

C:Accession: JN0085; A61515

R:Vasanthakumari, G.; Davis Jr., R.L.; Sullivan, M.A.; Donahue, J.P.

Gene 91, 63-69, 1990

A:Title: Cloning and expression in Escherichia coli of a hypoxanthine-guanine phosphorib

A:Reference number: JN0085; MUID:90382699; PMID:2205541

A:Accession: JN0085

A:Molecule type: mRNA

A:Residues: 1-231 <VAS>

A:Cross-references: EMBL:X16279

R:Kudson, C.

Mol. Biochem. Parasitol. 29, 125-132, 1988

A:Title: Isolation and partial characterisation of a 26 kilodalton antigen from Plasmodi

A:Reference number: A61515; MUID:88318789; PMID:3045539

A:Accession: A61515

A:Molecule type: protein

A:Residues: 2-20 <KID>

C:Superfamily: hypoxanthine phosphoribosyltransferase

C:Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 39.9%; Score 445.5; DB 2; Length 231;

Best Local Similarity 42.7%; Pred. No. 2.1e-30;

Matches 93; Conservative 40; Mismatches 74; Indels 11; Gaps 3;

Qy 5 SPGV-----VIMDDWPGYDNLNLTYPQHYGDLLEYVLIPHGIIVDRIERIAKDIMDI 57

Db 6 NPGAGENAFDPVFVKKDDGDLSEPMIAHYKKYLTVLVPNGVIKNRIEKLAYDIKKVY 65

Qy 58 GYSIDIMVLCKGGYKFCADLVEHLKNTSRNSDRFVSMKV---DFIRLKSVDNDOSMGEM 114

Db 66 NNEEPIICLLKXGSGFFTALLKHLRSIRHNSAVTSPKLFGEHYVRVAKSYCNDOSTGFL 125

Qy 115 QIIGGDLSTLAGKNFLIVEDVVGTRTMKALLSNIERYKPKMKIVASLLVKRTSRSGF 174

Db 126 EIV-SEDLSCLLKGKHLVIEDIITDKTLVKCFEYLVKFKFEIKTVAICLFIKETPLWNGF 184

Qy 175 RPYAGFIPIHLFVVGYSALDYNEYFRDLNHLICVINEHG 212

Db 185 KADFGVGSIPDHFVVGYSLDYNEIFRDLDHCLVNDG 222

RESULT 14

S66098

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) hprt - Bacillus subtilis

N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase hprt

C:Species: Bacillus subtilis

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S66098; B59642

R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.

DNA Res. 1, 1-14, 1994

A:Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom

A:Reference number: S65967; MUID:96051385; PMID:7584024

A:Accession: S66098

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180 <OGA>

A:Cross-references: EMBL:D26185; NID:g467326; PIDN:BA05303.1; PID:g467457

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C:Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, C.R.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler

tech, J.; Harwood, D.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Tosato, V.; Uchiyama

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69642

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-180 <KUN>

A:Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11894.1; PID:g2632335

A:Experimental source: strain 168

C:Genetics:

A:Gene: hprt

C:Superfamily: hypoxanthine phosphoribosyltransferase

C:Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 23.8%; Score 265.5; DB 2; Length 180;

Best Local Similarity 36.8%; Pred. No. 2.7e-15;

Matches 67; Conservative 35; Mismatches 63; Indels 17; Gaps 7;

Qy 31 DLEYVLPHGIIVDRIERIAKDIMKDIGYSIDIMVLC--VLKGGYKFCADLVEHLKKNISRN 88

Db 5 DIEKVLISEEEIQKKVKELGABLTSE--YQDTFPLAIGVLKGLPFMADLKH----- 56

Qy 89 SDRFVSMKVDFIRLKSVDNDQ--SMGEMOIIIGGDLST--LAGKNFLIVEDVVGTRTMKAL 146

Db 57 -DTYDEM--DFMDVSSYGNSTVSSGEVKII--KDLDTVEGRDILIEDIISGLTSLYL 111

Qy 147 LSNIEKYKPKMKIVASLLVKRTSRSDGPRPDYAGFEIPIHLFVVGYSALDYNEYFRDLNHLIC 206

Db 112 VELPRYRAKSIKIVTLLDKSGRKADIKADPVGEVPDAFVVGYSALDYNEYFRDLNHLIC 171

Qy 207 VI 208

Db 172 VL 173

RESULT 15

G86814

hypothetical protein hprt [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: G86814

R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: G86814

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180 <STO>

A:Cross-references: GB:AE005176; PID:gl2724518; PIDN:AAK05617.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: hprt

C:Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 23.8%; Score 265.5; DB 2; Length 180;

Best Local Similarity 35.4%; Pred. No. 2.7e-15;

Matches 64; Conservative 38; Mismatches 66; Indels 13; Gaps 4;

Qy 32 LEYVLPHGIIVDRIERIAKDIMKDIGYSIDIMVLCVKGKFCADLVEHLKKNISRNSDR 91

Db 5 LKEVLFTREQAERVKELAEVVSDEYGNPLVVGILKGSIMFTVDLLKELS----- 56

Qy 92 FVSMKVDFIRLKSVDNDQSMGEMOIIIGGDLSTLA--GKNFLIVEDVVGTRTMKALLSN 149

Db 57 -IDAEVDFMDVTSYGYGSISSSGEVRIL--KDLSTVAHGRDILIEDIIDTGTNTLLYLKLL 113

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 14:59:46 ; Search time 17 seconds
(without alignments)
586.451 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVVIMDDWPGYDLN.....LDYNEVFRDLNHCIVINEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	778	69.7	213	1 HPRT MUSSP	Q6431 mus spretus.
2	774	69.4	217	1 HPRT HUMAN	P00492 homo sapien
3	773	69.3	217	1 HPRT MOUSE	P00493 mus musculus
4	771	69.1	217	1 HPRT CRIGR	P00494 cricetus
5	771	69.1	217	1 HPRT MERUN	P47959 meriones un
6	768	68.8	218	1 HPRT RAT	P27605 rattus norv
7	753	67.5	218	1 HPRT CHICK	Q9w719 gallus gall
8	485	43.5	284	1 HPRT SCHMA	P09383 schistosoma
9	447.5	40.1	231	1 HGXR PLAFK	P20035 plasmodium
10	446.5	40.0	231	1 HGXR PLAFK	P07833 plasmodium
11	346	31.0	230	1 HGXR TOXGO	Q26997 toxoplasma
12	265.5	23.8	180	1 HPRT BACSU	P37472 bacillus su
13	261	23.4	183	1 HPRT LACLA	Q02522 lactococcus
14	255	22.8	178	1 HPRT AQUAE	Q66821 aquifex aeo
15	234.5	21.0	183	1 HGXR TRIFO	P51900 tritrichomo
16	232.5	20.8	202	1 HPRT MYCAV	P06794 mycobacteri
17	227.5	20.4	202	1 HPRT MYCTU	Q06383 mycobacteri
18	223.5	20.0	203	1 HPRT MYCLE	Q69537 mycobacteri
19	222.5	19.9	210	1 HPRT TRYBB	Q07010 trypanosoma
20	219	19.6	208	1 HPRT CRIFA	Q27541 crithidia f
21	218.5	19.6	211	1 HPRT LEIDH	P43152 leishmania
22	218.5	19.5	176	1 HPRT VIBHA	P18134 vibrio harv
23	216.5	19.4	178	1 HPRT ECOLI	P36766 escherichia
24	214.5	19.2	177	1 HPRT BUCAP	Q8K908 buchnera ap
25	209	18.7	182	1 HPRT RHOCAP	P37171 rhodobacter
26	204.5	18.3	178	1 HPRT SALTY	Q33799 salmonella
27	192	17.2	178	1 HPRT BUCAI	P57291 buchnera ap
28	189	16.9	179	1 HPRT HAEIN	P45078 haemophilus
29	160.5	14.4	175	1 HPRT MYCPN	P75119 mycoplasma
30	139.5	12.5	175	1 HPRT MYCGE	P47696 mycoplasma
31	137	12.3	180	1 PYRR_BACHD	Q8K9W4 bacillus ha
32	126.5	11.3	178	1 PYRR_ENTFA	Q52707 enterococcu
33	122.5	11.0	173	1 PYRR_STRPN	Q97qe1 streptococc

ALIGNMENTS

RESULT 1

ID	HPRT MUSSP	STANDARD;	PRT;	213 AA.
AC	Q64531;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPT)			
DE	(HGPTase) (HPRT A) (Fragment).			
GN	HPRT.			
OS	Mus spretus (Western wild mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10096;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Brain;			
RA	MEDLINE=88243783; PubMed=3379061;			
RX	Johnson G.G., Kroner W.A., Bernstein S.I., Chapman V.M., Smith K.D.;			
RT	"Altered turnover of allelic variants of hypoxanthine phosphoribosyltransferase is associated with N-terminal amino acid sequence variation."			
RL	J. Biol. Chem. 263:9079-9082(1988).			
CC	!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-			
CC	!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-			
CC	!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-			
CC	!- PATHWAY: Purine salvage.			
CC	!- SUBUNIT: Homotrimer (By similarity).			
CC	!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; M20011; AAA96234.1; -			
DR	PIR; I49758; I49758.			
DR	HSSP; P00492; 1B2V.			
DR	MGD; MGI:96217; Hprt.			
DR	InterPro; IPR005904; Hxn phspho trans.			
DR	InterPro; IPR002375; P1/PY_ID_Transf.			
DR	InterPro; IPR000936; PRTtransferase.			
DR	Pfam; PF00156; Pribosyltran; 1.			
DR	TIGRFAMs; TIGR01203; HGPTase; 1.			
DR	PROSITE; P500103; PUR PYR PR TRANSFER; 1.			
KW	Transferase; Glycosyltransferase; Purine salvage; Magnesium; Acetylation.			
KW	Acetylation.			
FT	INIT_MET 0 0			
FT	MOD_RES 1 1			
FT	METAL 133 133			
FT	ACETYLATION (PROBABLE).			
FT	MAGNESIUM (BY SIMILARITY).			

34	121	10.8	178	1	PYRR_CLOAB	Q97ha0 clostridium
35	120.5	10.8	178	1	PYRR_THETN	Q87r3 thermoanaer
36	119	10.7	178	1	PYRR_CLOPE	Q8xjb2 clostridium
37	117	10.5	192	1	PYRR_CORGL	P59011 corynebacte
38	116.5	10.4	180	1	PYRR_ANASL	Q8yv98 anabaena sp
39	116	10.4	180	1	PYRR_LACPL	P71479 lactobacill
40	116	10.4	193	1	PYRR_STRCO	Q9kxri streptomyce
41	115.5	10.3	178	1	PYRR_SYNY3	Q85758 synechocyst
42	114.5	10.3	173	1	PYRR_STRP3	Q8k7y5 streptococc
43	114.5	10.3	173	1	PYRR_STRPY	Q9a0d0 streptococc
44	113.5	10.2	179	1	PYRR_HASIN	P44722 haemophilus
45	111.5	10.0	173	1	PYRR_STRP8	P59013 streptococc

FT METAL 134 134 MAGNESIUM (BY SIMILARITY).
 FT NON TER 213 213
 SQ SEQUENCE 213 AA; 23950 MW; 8844851C8BC50BE8 CRC64;
 Query Match 69.7%; Score 778; DB 1; Length 213;
 Best Local Similarity 68.7%; Pred. No. 5.6e-58;
 Matches 145; Conservative 31; Mismatches 35; Indels 0; Gaps 0;
 QY 2 ATRSPGVIMDDWPGYDLNLTYPQHYGDELYVLIPIPHGIIIVDRIERLAKDWMKQIGYSD 61
 DB 1 ATRSPSVVISDEPGYDLDFCIENHYVEDLEKVPFPHGLMDRTERLARDVWKGNGHH 60
 QY 62 IMVLCKGKYKFCADLVHKLKNISSNRDRFVSMKVDFIRLKSYNQDQMGEMQIIGGD 121
 DB 61 IVALCVLKGKYKFCADLVHKLKNISSNRDRFVSMKVDFIRLKSYNQDQMGEMQIIGGD 120
 QY 122 LSTLAKGNFLIYEDVVGTGRTKALLSNETKYPKNMKVASLLVVKRTSSDGRPDYAGF 181
 DB 121 LSTLTKGNVLIYEDVIDTQKTQTLISLVKQSPKMKVASLLVVKRTSSVGRPRDFVGF 180
 QY 182 EIPHLFVVGVALDYNEYFRDLNHLICVINEHG 212
 DB 181 EIPDKFVVGVALDYNEYFRDLNHLVHCVISETG 211
 RESULT 2
 HPRT HUMAN
 ID HPRT HUMAN STANDARD; PRT; 217 AA.
 AC P00492;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPR)
 DE (HGPRase).
 GN HPRT1 OR HPRT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82265815; PubMed=7107641;
 RA Wilson J.M., Tarr G.E., Mahoney W.C., Kelley W.N.;
 RT "Human hypoxanthine-guanine phosphoribosyltransferase. Complete amino
 acid sequence of the erythrocyte enzyme.";
 RL J. Biol. Chem. 257:10978-10985(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83169681; PubMed=6300847;
 RA Jolly D.J., Okayama H., Berg P., Esty A.C., Filpula D., Bohlen P.,
 RA Johnson G.G., Shively J.E., Hunkapiller T., Friedmann T.;
 RT "Isolation and characterization of a full-length expressible cDNA for
 human hypoxanthine phosphoribosyl transferase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:477-481(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90256168; PubMed=2341149;
 RA Edwards A., Voss H., Rice P., Civitello A., Stegemann J.,
 RA Schwager C., Zimmermann J., Erle H., Caskey C.T., Ansorge W.;
 RT "Automated DNA sequencing of the human HPRT locus.";
 RL Genomics 6:593-608(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-8 FROM N.A.
 RX MEDLINE=87064322; PubMed=3023844;
 RA Patel P.I., Framson P.E., Caskey C.T., Chinnault A.C.;
 RT "Fine structure of the human hypoxanthine phosphoribosyltransferase
 gene.";
 RL Mol. Cell. Biol. 6:393-403(1986).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RX MEDLINE=94320143; PubMed=8044844;
 RA Bads J.C., Scapin G., Xu Y., Grubmeyer C., Sacchettini J.C.;
 RT "The crystal structure of human hypoxanthine-guanine
 phosphoribosyltransferase with bound GMP.";
 RL Cell 78:325-344(1994).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=99287111; PubMed=10360366;
 RA Shi W., Li C.M., Tyler P.C., Furneaux R.H., Grubmeyer C.,
 RA Schramm V.L., Almo S.C.;
 RT "The 2.0 Å structure of human hypoxanthine-guanine
 phosphoribosyltransferase in complex with a transition-state analog
 inhibitor.";
 RL Nat. Struct. Biol. 6:588-593(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=99268335; PubMed=10338013;
 RA Balendiran G.K., Molina J.A., Xu Y., Torres-Martinez J., Stevens R.,
 RA Focia P.J., Eakin A.E., Sacchettini J.C., Craig S.P. III;
 RT "Ternary complex structure of human HGPRTase, PRPP, Mg2+, and the
 inhibitor HPP reveals the involvement of the flexible loop in
 substrate binding.";
 RL Protein Sci. 8:1023-1031(1999).
 RN [9]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=93138599; PubMed=1487231;
 RA Sculley D.G., Dawson P.A., Emmerson B.T., Gordon R.B.;
 RT "A review of the molecular basis of hypoxanthine-guanine
 phosphoribosyltransferase (HGPRT) deficiency.";
 RL Hum. Genet. 90:195-207(1992).
 RN [10]
 RP VARIANT TORONTO.
 RX MEDLINE=83213351; PubMed=6853490;
 RA Wilson J.M., Kobayashi R., Fox I.H., Kelley W.N.;
 RT "Human hypoxanthine-guanine phosphoribosyltransferase.";
 RL J. Biol. Chem. 258:6458-6460(1983).
 RN [11]
 RP VARIANT KINSTON.
 RX MEDLINE=83213940; PubMed=6853716;
 RA Wilson J.M., Kelley W.N.;
 RT "Molecular basis of hypoxanthine-guanine phosphoribosyltransferase
 deficiency in a patient with the Lesch-Nyhan syndrome.";
 RL J. Clin. Invest. 71:1331-1335(1983).
 RN [12]
 RP VARIANT LONDON.
 RX MEDLINE=83144031; PubMed=6572373;
 RA Wilson J.M., Tarr G.E., Kelley W.N.;
 RT "Human hypoxanthine (guanine) phosphoribosyltransferase: an amino
 acid substitution in a mutant form of the enzyme isolated from a
 patient with gout.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:870-873(1983).
 RN [13]

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```

CC EMBL; J00423; AA96232.1; -.
CC EMBL; K01515; AA96271.1; -.
CC EMBL; K01507; AA96271.1; JOINED.
CC EMBL; K01508; AA96271.1; JOINED.
CC EMBL; K01509; AA96271.1; JOINED.
CC EMBL; K01510; AA96271.1; JOINED.
CC EMBL; K01511; AA96271.1; JOINED.
CC EMBL; K01512; AA96271.1; JOINED.
CC EMBL; K01513; AA96271.1; JOINED.
CC EMBL; K01514; AA96271.1; JOINED.
CC PIR; I49756; RTMSG.
CC HSP; P00492; LHMP.
CC MGD; MGI.96217; Hprt.
CC InterPro; IPR005904; Hxn_pshpho_trans.
CC InterPro; IPR002375; Pr/py_ip_transf.
CC InterPro; IPR000836; PRTtransferase.
CC Pfam; PF00156; Priboyltran; 1.
CC TIGRfams; TIGR01203; HGPRTase; 1.
CC PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT INIT_MET 0
FT METAL 133 133 MAGNESIUM (BY SIMILARITY).
FT METAL 134 134 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 200 200 D -> N (IN REF. 1).
SQ SEQUENCE 217 AA; 24439 MW; A21CCD4DB64693B5 CRC64;

Query Match 69.3%; Score 773; DB 1; Length 217;
Best Local Similarity 68.6%; Pred. No. 1.5e-57;
Matches 144; Conservative 31; Mismatches 35; Indels 0; Gaps 0;

Qy 3 TRSPGVIMDDPFGYDLNLFYQHYGDLVYLPHGIIIVDRIBRLAKDIMKDIGSDI 62
Db 2 TRSFVVISDDEPGYDLDFCIPNHAYEDLEKVFIPHGLIMDRTERLARDVMKGGHHI 61
Qy 63 MVLCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGGDL 122
Db 62 VALCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSGTGDIKIVGGDL 121
Qy 123 STLAKGNFLIVEDVGTGRTMKALLSNIEKYKPNMIKVASLLVKRTSRSDGPRPDYAGFE 182
Db 122 STLTGKNVLIVEDIIDTGKTMQTLTLLSKVQSPKMKVVASLLVKRTSRSGVGRDFVGFE 181
Qy 183 IPHLVFVGVYALDYNEFYFDLNHCIVNEHG 212
Db 182 IPDKFVGVYALDYNEFYFDLNHCIVNEHG 211

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RESULT 4
HPRT CRIGR ID HPRT CRIGR STANDARD; PRT; 217 AA.
AC P00494;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)
GN HGPRTase.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9116526; PubMed=2004774;
RA Rossiter B.J.F., Fuscoe J.C., Muan D.M., Fox M., Caskey C.T.;
RT "The Chinese hamster HPRT gene: restriction map, sequence analysis, and multiplex PCR deletion screen.";

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RL Genomics 9:247-256(1991).
RN [2]
RX MEDLINE=83090437; PubMed=6294614;
RA Konecki D.S., Brennan J., Fuscoe J.C., Caskey C.T., Chinault A.C.;
RT "Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hamster: construction and sequence analysis of cDNA recombinants.";
RL Nucleic Acids Res. 10:6763-6775(1982).
CC -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: Purine salvage.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THE CELL LINES FROM WHICH THIS SEQUENCE WAS CLONED ARE REVERTANTS FROM MUTANTS WITH NO DETECTABLE ENZYME ACTIVITY. THE PHENOTYPIC REVERSIONS ARE THE RESULT OF OVERPRODUCTION OF VARIANT ENZYMES BECAUSE OF GENE AMPLIFICATION. THIS VARIANT SEQUENCE IS EXPECTED TO BE VERY SIMILAR TO THE WILD TYPE.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.

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CC EMBL; X53073; CAA37247.1; -.
CC EMBL; X53074; CAA37247.1; JOINED.
CC EMBL; X53075; CAA37247.1; JOINED.
CC EMBL; X53076; CAA37247.1; JOINED.
CC EMBL; X53077; CAA37247.1; JOINED.
CC EMBL; X53078; CAA37247.1; JOINED.
CC EMBL; X53079; CAA37247.1; JOINED.
CC EMBL; X53080; CAA37247.1; JOINED.
CC EMBL; J00060; AAA36990.1; -.
CC PIR; S14402; RTHYG.
CC HSP; P00492; LHMP.
CC InterPro; IPR005904; Hxn_pshpho_trans.
CC InterPro; IPR002375; Pr/py_ip_transf.
CC InterPro; IPR000836; PRTtransferase.
CC Pfam; PF00156; Priboyltran; 1.
CC TIGRfams; TIGR01203; HGPRTase; 1.
CC PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT INIT_MET 0
FT METAL 133 133 MAGNESIUM (BY SIMILARITY).
FT METAL 134 134 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 217 AA; 24512 MW; 119A67BF990F88A1 CRC64;

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Query Match 69.1%; Score 771; DB 1; Length 217;
Best Local Similarity 68.7%; Pred. No. 2.2e-57;
Matches 145; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

Qy 2 ATRSPGVIMDDPFGYDLNLFYQHYGDLVYLPHGIIIVDRIBRLAKDIMKDIGSD 61
Db 1 ATRSFVVISDDEPGYDLDFCIPNHAYEDLEKVFIPHGLIMDRTERLARDVMKGGHH 60
Qy 62 IMVLCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGGDL 121
Db 61 IVALCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSGTGDIKIVGGDL 120
Qy 122 LSTLAGKNFLIVEDVGTGRTMKALLSNIEKYKPNMIKVASLLVKRTSRSDGPRPDYAGFE 181
Db 121 LSTLTGKNVLIVEDIIDTGKTMQTLTLLSKVQSPKMKVVASLLVKRTSRSGVGRDFVGFE 180
Qy 182 EIPHLFVGVYALDYNEFYFDLNHCIVNEHG 212

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Db      181 EIPDKFVGVGYALDYNEFRDLNHCIVISGTG 211
RESULT 5
HPRT MERUN STANDARD; PRT; 217 AA.
AC PA7959;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRPT)
DE (HGPRPTase).
GN HPRT.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OC NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=9918980; PubMed=10090010;
RA Mai Z., Horobov D.W., Klei T.R.;
RT "Hypoxanthine phosphoribosyltransferase cDNA in gerbils (Meriones unguiculatus)".
RL Lab. Anim. Sci. 48:179-183(1998).
CC -1- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -1- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: Purine salvage.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
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CC -----
DR EMBL; L37778; AAA65676.1; -
DR HSSP; P00492; 1BZY.
DR InterPro; IPR005904; Hxn_phspo_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Pribsyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRPTase; 1.
DR PROSITE; PS00103; PUR_PIR_PR_TRANSFER; 1.
DR TRANSFERASE; Glycosyltransferase; Purine salvage; Magnesium.
FT INIT_MET 0
FT METAL 133 133 MAGNESIUM (BY SIMILARITY).
FT METAL 134 134 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 217 AA; 24407 MW; 68DC5D9397A8144C CRC64;
Query Match 69.1%; Score 771; DB 1; Length 217;
Best Local Similarity 67.3%; Pred. No. 2.2e-57;
Matches 142; Conservative 34; Mismatches 35; Indels 0; Gaps 0;
QY 2 ATRSPGVVIMDDWPGYDLNLFYPOHYGDLVEYVLPHGIIVDRIERLAKDIMKDIGYSD 61
Db 1 ATRSPSIVIGDDEFGYDLDLCIPKHYAEDLEKVFIPHGLIMDRTERLARDVMKMGHH 60
QY 62 IMVLVLKGGYKFCADLVEHUKNISRSNDRFVSMKVFIRLKSRYNRDQSGMGEMQIIIGGD 121
Db 61 IVALCVLKGKGFADLLDYIKSLNRNDRSGIPMTVDIFIRLKSVCNQDQSGIDIKVIGDD 120
QY 122 LSTLAGKNFLVEDVVGTRTKMALLNIEKYKPNMLKVASLAVKRTSRSDGFRPDYAGF 181
Db 121 LSALTGRKNVLIEDIIDTKMTQTLISLVQKISFQKVASLLVTRTPRSVGVRPDPVGF 180

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QY 182 EIPHLFVVGVGYALDYNEFRDLNHCIVINEHG 212
Db 181 EIPDKFVGVGYALDYNEFRDLNHCIVISEG 211
RESULT 6
HPRT RAT STANDARD; PRT; 218 AA.
AC P27605; O62926;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRPT)
DE (HGPRPTase).
GN HPRT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147115; PubMed=1783384;
RA Chiaverotti T.A., Battula N., Monnat R.J. Jr.;
RT "Rat hypoxanthine phosphoribosyltransferase cDNA cloning and sequence analysis."
RL Genomics 11:1158-1160(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92142869; PubMed=1781355;
RA Chiaverotti T.A., Battula N., Monnat R.J. Jr.;
RT "Rat hypoxanthine phosphoribosyltransferase cDNA cloning and sequence analysis."
RL Adv. Exp. Med. Biol. 309B:117-120(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Jansen J., Vrieling H., van Zeeland A., Mohn G.;
RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344; TISSUE=Spleen;
RA Chen T., Mittelsaet R.A., Heflich R.H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -1- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: Purine salvage.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63983; AAA41350.1; -
DR EMBL; S79292; AAB21288.1; -
DR EMBL; X62085; CAA43997.1; -
DR EMBL; AF001282; AAB65640.1; -
DR EMBL; AF001278; AAB65640.1; JOINED.
DR EMBL; AF009655; AAB65640.1; JOINED.
DR EMBL; AF009656; AAB65640.1; JOINED.
DR EMBL; AF001279; AAB65640.1; JOINED.
DR EMBL; AF001280; AAB65640.1; JOINED.
DR EMBL; AF001281; AAB65640.1; JOINED.
DR FIR; S18140; S18140.
DR HSSP; P00492; 1HMP.

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DR	EMBL; AJ132697; CAB46657.1; -.
DR	HSSP; P00492; IHMP.
DR	InterPro; IPR005904; Hxn_pshpo trans.
DR	InterPro; IPR002375; Pr/PY_xp.transf.
DR	InterPro; IPR000836; PRtransferase.
DR	Pfam; PF00156; Pfribosyltran; 1.
DR	TIGRFAMs; TIGR01203; HGPRTase; 1.
DR	PROSITE; PS00103; PUR_Pyr_PR_TRANSFER; 1.
KW	Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT	METAL 134 134 MAGNESIUM (BY SIMILARITY).
FT	METAL 135 135 MAGNESIUM (BY SIMILARITY).
SQ	SEQUENCE 218 AA; 24x08 MW; 2228B84B0B6AF727 CRC64;
Query Match 67.5%; Score 753; DB 1; Length 218;	
Best Local Similarity 67.0%; Pred. No. 6.9e-56;	
Matches 142; Conservative 32; Mismatches 38; Indels 0; Gaps 0;	
Qy	1 MATRSPGVIMDWPGVDLNLFFYPQHYYGDLEVLPHGLIVDRIERLANDIKMDICYS 60
Dd	1 MATHSPCIVGDDGGQYDLDFCIPKHYADBLEKVYPHGLIMDRTERLARIEIKMGMGH 60
Qy	61 DIWLVCVLKGKYKFCADLVHLKNISRSNDRFVSMKVDYFLRLKSRYNDOSGMQIIIGG 120
Dd	61 HIVALCVLKGGYKFADLDLYIKALNNRSDSKSIPMTVDYFLRLKSYCNDSQSGDIKVGGD 120
Qy	121 DLSTLAGKNFLIVEDVVGTGRTKALLSNIEKYKPNMKVASLLVKRTSRSDGFRPDYAG 180
Dd	121 DLSTLTGKNVLIVEDIIDTCKTKMLLSLLKQYNPKMVKVASLLVKRTPSRVGYRPDPFG 180
Qy	181 FEIPHLFVUGYALDYNEYFRDLNHICVINEHG 212
Dd	181 FEVPDKFWGYALDYNEYFRDLNHICVISETG 212
RESULT 8	
ID	HPRT_SCHMA STANDARD; PRT; 284 AA.
AC	P09383;
DT	01-MAR-1989 (Rel. 10, Created)
DT	01-MAR-1989 (Rel. 10, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPR1)
DE	(HGPRtase).
GN	HGPR1.
OS	Schistosoma mansoni (Blood fluke).
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC	Schistosomatoidea; Schistosomatidae; Schistosoma.
OX	NCBI_TaxID=6183;
RX	[1]
RC	SEQUENCE FROM N.A.
RC	STRAIN=Puerto Rican;
RX	MEDLINE=88303331; PubMed=3136439;
RA	Craig S.P., McKerrow J.H., Newport G.N., Wang C.C.;
RA	"Analysis of cDNA encoding the hypoxanthine-guanine
RT	phosphoribosyltransferase (HGPRtase) of Schistosoma mansoni; a
RT	putative target for chemotherapy.";
RL	Nucleic Acids Res. 16:7087-7101(1988).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Puerto Rican;
RX	MEDLINE=89160320; PubMed=2701934;
RA	Craig S.P., Muralidhar M.G., McKerrow J.H., Wang C.C.;
RT	"Evidence for a class of very small introns in the gene for
RT	hypoxanthine-guanine phosphoribosyltransferase in Schistosoma
RT	mansoni.";
RL	Nucleic Acids Res. 17:1635-1647(1989).
-!	CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC	alpha-D-ribose 1-diphosphate.
-!	CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC	alpha-D-ribose 1-diphosphate.
-!	PATHWAY: Purine salvage.
-!	SUBUNIT: Homotetramer (By similarity).
-!	SUBCELLULAR LOCATION: Cytoplasmic.


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FT TURN 179 180
FT STRAND 185 185
FT STRAND 188 193
FT STRAND 198 200
FT TURN 201 202
FT STRAND 203 203
FT STRAND 205 205
FT TURN 206 207
FT STRAND 208 208
FT TURN 210 211
FT STRAND 215 218
FT STRAND 220 225
FT TURN 226 226
FT SEQUENCE 231 AA; 26348 MW; 4E681B63FD3D8131 CRC64;

Query Match 40.1%; Score 447.5; DB 1; Length 231;
Best Local Similarity 42.7%; Pred. No. 2.2e-30;
Matches 93; Conservative 41; Mismatches 73; Indels 11; Gaps 3;

QY 5 SPGV-----VIMDDWPGYDLMLFTYPOHYGDLVYLPHGIIIVDRIERLAKDIMKDI 57
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 65
QY 58 GYSDIMVLGVKGGYKFCADLVEHLKNIISRNDRFVSMKV---DFIRLKSRYNDQSMGEM 114
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 125
QY 115 QIIGGSDLSTLAKGNFLIVEDVVGRTMKALLSNIEKYKPNMIKVASLLVKTSTRSDGF 174
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 184
QY 175 RPDYAGFEIPLHVVVGYALDYNEFRDLNHCIVINEHG 212
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 222

RESULT 10
HGXR_PLAFK STANDARD; PRT; 231 AA.
AC P07833;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine-xanthine phosphoribosyltransferase (EC 2.4.2.-)
DE (HGXPRT) (HGXPRTase) (HGPRRT).
GN LACZ.
OS Plasmodium falciparum (isolate K1 / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5839;
RN [1]_TaxID=5839;
RP SEQUENCE FROM N.A.
RX MEDLINE=88096579; PubMed=3320967;
RA King A., Melton D.W.;
RT "Characterisation of cDNA clones for hypoxanthine-guanine phosphoribosyltransferase from the human malarial parasite, Plasmodium falciparum: comparisons to the mammalian gene and protein."
RL Nucleic Acids Res. 15:10469-10481(1987).
CC -!- FUNCTION: WORKS WITH GUANINE, HYPOXANTHINE AND XANTHINE.
CC -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- CATALYTIC ACTIVITY: 5-phospho-alpha-D-ribose 1-diphosphate +
CC xanthine = (9-D-ribose) xanthine)-5'-phosphate + phosphate.
CC -!- PATHWAY: Purine salvage.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00519; CA68573.1; -.
DR PIR; S06315; S06315.
DR HSSP; P20035; 1CJB.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/PY_rD_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRfams; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT METAL 144 144 MAGNESIUM (BY SIMILARITY).
FT METAL 145 145 MAGNESIUM (BY SIMILARITY).
FT SEQUENCE 231 AA; 26392 MW; A350333D5F5DD287 CRC64;

Query Match 40.0%; Score 446.5; DB 1; Length 231;
Best Local Similarity 42.7%; Pred. No. 2.6e-30;
Matches 93; Conservative 41; Mismatches 73; Indels 11; Gaps 3;

QY 5 SPGV-----VIMDDWPGYDLMLFTYPOHYGDLVYLPHGIIIVDRIERLAKDIMKDI 57
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 65
QY 58 GYSDIMVLGVKGGYKFCADLVEHLKNIISRNDRFVSMKV---DFIRLKSRYNDQSMGEM 114
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 125
QY 115 QIIGGSDLSTLAKGNFLIVEDVVGRTMKALLSNIEKYKPNMIKVASLLVKTSTRSDGF 174
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 184
QY 175 RPDYAGFEIPLHVVVGYALDYNEFRDLNHCIVINEHG 212
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 222

RESULT 11
HGXR_TOXGO STANDARD; PRT; 230 AA.
AC Q26997;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypoxanthine-guanine-xanthine phosphoribosyltransferase (EC 2.4.2.-)
DE (HGXPRT) (HGXPRTase) (HGPRRT).
GN HPRT.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]_TaxID=5811;
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RX MEDLINE=94374703; PubMed=8088544;
RA Vasanthakumar G., van Ginkel S., Parish G.;
RT "Isolation and sequencing of a cDNA encoding the hypoxanthine-guanine
RT phosphoribosyltransferase from Toxoplasma gondii."
RL Gene 147:153-154(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.4 AND 2.9 ANGSTROMS).
RX MEDLINE=96433078; PubMed=8836106;
RA Schumacher M.A., Carter D., Roos D.S., Ullman B., Brennan R.G.;
RT "Crystal structures of Toxoplasma gondii HGXPRTase reveal the
RT catalytic role of a long flexible loop."
RL Nat. Struct. Biol. 3:881-887(1996).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=20014541; PubMed=10545170;

```


RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haleck J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno K., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Burnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger W., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleicher S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Solido B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
CC -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: Purine salvage.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.

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DR EMBL; D26185; BAA0303.1; -;
DR EMBL; Z99104; CAB11844.1; -;
DR PIR; S66098; S66098.
DR HSSP; P51900; LHGX.
DR Subtilist; BG10131; hprt.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR Transferase; Glycosyltransferase; Purine salvage; Magnesium;
KW Complete proteome.
FT METAL 99 99 MAGNESIUM (BY SIMILARITY).
FT METAL 100 100 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 180 AA; 20239 MW; 5D247BB64A57D92 CRC64;
Query Match 23.8%; Score 265.5; DB 1; Length 180;
Best Local Similarity 36.8%; Pred. No. 2.4e-15;
Matches 67; Conservative 35; Mismatches 63; Indels 17; Gaps 7;
31 DLEYVLPHGIIIVDRTERLAKDIMKIDIGYSDIMVLC--VLKGYKFCADLVEHLKKNISRN 88
5 DIEKVLISSEETQKKVKELGAEITST--YDFTFPLAIGLVKALPMPADLKHII----- 56
89 SDRFVSMKVDFIRLKSRYNDQ-SMGEMQIIGGDLST-LAGKNFLIVEDVGTGRTMKAL 146
57 -DTYLEM--DFMDVSYGNSVTSSGEVKII--KDLTSTVEGRDILLIEDISGLTSLYL 111
147 LSNIKEYKPMKIVASLLLYKRTSRSDGPRPDYAGEIPIHLFVVGVYALDYNEFRDINHIC 206
112 VELFRYKAKSIKIVTLDDKPSGRKADIKAFVGEVFPDAFVVGGLDYAERYNLPYIG 171

QY 207 VI 208
DB 172 VL 173
RESULT 13
HPRT LACLA STANDARD; PRT; 183 AA.
AC Q02522;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)
DE (HGPRTase).
GN HPT OR LL0020.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHCC285;
RX MEDLINE=93101141; PubMed=1465108;
RA Nilsson D., Lauridsen A.A.;
RT "Isolation of purine auxotrophic mutants of Lactococcus lactis and
RT characterization of the gene hpt encoding hypoxanthine guanine
RT phosphoribosyltransferase.";
RL Mol. Gen. Genet. 235:359-364(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis LL1403".
RL Genome Res. 11:731-753(2001).
CC -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: Purine salvage.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.

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DR EMBL; X67015; CAA47404.1; -;
DR EMBL; X69123; CAA48876.1; -;
DR EMBL; AE006241; AAK04118.1; -;
DR PIR; D86627; D86627.
DR PIR; S30100; S30100.
DR HSSP; P00492; 1HMP.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR Transferase; Glycosyltransferase; Purine salvage; Magnesium;
KW Complete proteome.
FT METAL 103 103 MAGNESIUM (BY SIMILARITY).
FT METAL 104 104 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 183 AA; 20648 MW; A9D903FC9E6EBDB7 CRC64;
Query Match 23.4%; Score 261; DB 1; Length 183;

RESULT 14	HPRT_AQUAE	STANDARD;	PRT;	178 AA.
AC	O66821;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPR)			
DE	(HGPRase)			
GN	HPT OR AQ 544.			
OS	Aquifex aeolicus.			
OC	Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.			
OX	NCBI_TaxID=63363;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=VF5;			
RX	MEDLINE=98196666; PubMed=9537320;			
RA	Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,			
RA	Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,			
RA	Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;			
RT	"The complete genome of the hyperthermophilic bacterium Aquifex			
RT	aeolicus";			
RL	Nature 392:353-358(1998).			
CC	-!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-			
CC	alpha-D-ribose 1-diphosphate.			
CC	-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-			
CC	alpha-D-ribose 1-diphosphate.			
CC	-!- PATHWAY: Purine salvage.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE			
CC	PHOSPHORIBOSYLTRANSFERASE FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AE000695; AAC06788.1; -.			
DR	PIR; A70349; A70349.			
DR	HSP; P00492; IMP.			
DR	InterPro; IPR005904; Hxn_phspb trans.			
DR	InterPro; IPR002375; Pr/PY_rdp trans.			
DR	InterPro; IPR000836; PRtransferase.			
DR	Pfam; PF00156; Pribosyltran; 1.			
DR	TIGfam; TIGR01203; HGPRase; 1.			
DR	PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.			
KW	Transferase; Glycosyltransferase; Purine salvage; Magnesium;			
KW	Complete proteome.			
FT	METAL 102 102 MAGNESIUM (BY SIMILARITY).			
FT	METAL 103 103 MAGNESIUM (BY SIMILARITY).			
SEQUENCE	178 AA; 20628 MW; CBB889459690538 CRC64;			
Query Match	22.8%; Score 255; DB 1; Length 178;			
Best Local Similarity	34.8%; Pred. No. 1.8e-14;			

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DR EMBL; L08622; AAC37202.1; -.
DR PDB; 1HGX; 17-AUG-96.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PMtransf_kase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium;
KW 3D-structure.
FT METAL 102 102 MAGNESIUM.
FT METAL 103 103 MAGNESIUM.
FT TURN 8 9
FT STRAND 10 15
FT HELIX 17 35
FT TURN 36 38
FT STRAND 41 45
FT TURN 46 49
FT HELIX 50 57
FT TURN 58 59
FT STRAND 65 72
FT STRAND 87 87
FT TURN 94 95
FT STRAND 97 105
FT HELIX 109 119
FT TURN 120 121
FT STRAND 125 134
FT STRAND 147 152
FT STRAND 157 159
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FT STRAND 162 162
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FT TURN 165 166
FT STRAND 167 167
FT TURN 169 170
FT STRAND 174 177
FT HELIX 179 183
SQ SEQUENCE 183 AA; 21091 MW; A151E2FSD7D1C214 CRC64;

Query Match 21.0%; Score 234.5; DB 1; Length 183;
Best Local Similarity 32.4%; Pred.No.9.se-13;
Matches 59; Conservative 37; Mismatches 73; Indels 13; Gaps 4;
QY 31 DLEYVLIPHGIIVDRIERLAKDIMKDIGYSDIMVLCLVKGKFCADLVEHLKNISRNSD 90
Db 9 DLERVLYNQDDIQKRIRELAELTEFYEDKNPNVICVLTGAVFFYTDLEKHLD----- 61
QY 91 RFVSMKVDIFRLKSYRNDOSMGEMQIIGGGDLST-LAGKNFLIVEDVVGTRMTKALLSN 149
Db 62 --FQLEPDVVICSSYSGTKSTGNLT--SKDLKTNIEGRHVLAVVEDIIDTGLTMYQLNN 117
QY 150 IEKYKPNMKVASLLVKRTSRDGRFP-DYAGFEIPLHFWGVYALDYNEFYFDLNLHICVI 208
Db 118 LQMRKPEASIKVCTCDKDGKAYDVPIDYCGFVVENRYIIGYGFDFHKNYRNLFPVIGIL 177
QY 209 NE 210
Db 178 KE 179

Search completed: November 13, 2003, 15:05:31
Job time : 18 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 15:02:56 ; Search time 35 Seconds
(without alignments)
1563.061 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVVIMDDPGVDLN.....LDYNEYFRDLNHCIVINEHG 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1065	95.4	225	Q09RG1	Q09rg1 homo sapien
2	786	70.4	218	Q60466	Q60466 cricetus
3	782	70.1	218	Q09KF5	Q09kf5 mus musculus
4	779	69.8	218	Q64401	Q64401 cricetus
5	746	66.8	210	Q09JK76	Q09jk76 akodon curs
6	658	59.0	186	Q09JIT9	Q09jit9 bos taurus
7	553	43.6	161	Q09JK75	Q09jk75 akodon curs
8	543	48.7	154	Q46381	Q46381 coryctolagus
9	470	42.1	142	Q09XS14	Q09xs14 sus scrofa
10	456	40.9	135	Q28968	Q28968 sus scrofa
11	455	40.8	193	Q28530	Q28530 macropus ro
12	445.5	40.0	231	Q086085	Q086085 plasmodium
13	445.5	39.9	231	Q081JUS1	Q081j1 plasmodium
14	437	39.2	136	Q095258	Q095258 sus scrofa
15	430.5	38.6	214	Q09NF11	Q09nf11 caenorhabdi
16	400	35.8	194	Q03925	Q03925 plasmodium

17	346	31.0	279	5	Q27375	Q27375 toxoplasma
18	306	27.4	84	6	Q29494	Q29494 macropus to
19	294	26.3	85	6	P79306	P79306 sus scrofa
20	290.5	26.0	115	11	O55061	O55061 mesocricetu
21	272	24.4	76	6	O97876	O97876 ornithorhyn
22	270.5	24.2	183	16	Q8XHL2	Q8xhl2 clostridium
23	265.5	23.8	180	16	Q9CFP9	Q9cff9 lactococcus
24	265	23.7	76	6	O97875	O97875 monodelphis
25	265	23.7	76	6	O97873	O97873 macropus eu
26	265	23.7	76	6	O97872	O97872 isodon mac
27	257.5	23.1	178	16	O97EB1	O97eb1 clostridum
28	257.5	23.1	180	16	Q8P321	Q8p321 streptococc
29	257	23.0	176	16	Q8KC97	Q8kc97 chlorobium
30	254.5	22.8	648	16	Q92F56	Q92f56 listeria in
31	252	22.6	76	6	O97871	O97871 isodon mac
32	251.5	22.5	181	16	Q8R710	Q8r710 thermoanaer
33	251.5	22.5	194	16	Q8NM82	Q8nm82 corynebacte
34	250.5	22.4	648	2	Q8KU03	Q8ku03 listeria mo
35	250.5	22.4	648	16	Q8YAC7	Q8yac7 listeria mo
36	247.5	22.2	180	16	Q97TC4	Q97tc4 streptococc
37	247.5	22.2	180	16	Q8DRP8	Q8drp8 streptococc
38	246.5	22.1	184	16	Q8EUI7	Q8eul7 oceanobacil
39	246	22.0	175	16	Q8RGK5	Q8rgk5 fusobacteri
40	245	22.0	76	6	O97874	O97874 macropus eu
41	244.5	21.9	175	2	Q9ZNK6	Q9zmk6 clostridium
42	242.5	21.7	238	5	Q95ZC9	Q95zc9 leishmania
43	241	21.6	212	16	Q8FMG1	Q8fmgl corynebacte
44	239.5	21.5	179	16	Q99W93	Q99w93 staphylococ
45	239	21.4	241	5	Q9U6Y2	Q9u6y2 leishmania

ALIGNMENTS

RESULT 1

Q09RG1 PRELIMINARY; PRT; 225 AA.
AC Q09RG1
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE HHGP (HHGP protein).
GN HHGP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver cancer;
RA Li Y., Wu T., Xu S., Ren S., Chen Z., Han Z.;
RT "A novel gene expressed in human liver cancer tissue."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NED0 human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226056; AAF86956.1; -;
DR EMBL; AK021950; BAB13944.1; -;
DR EMBL; BC008662; AAH08662.1; -;
DR HSSP; P00492; 1HMP.
DR InterPro; IPR005904; Hxn_phospho_trans.

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DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
KW Transferase
SQ SEQUENCE 225 AA; 25673 MW; CD612C2783AC3071 CRC64;
Query Match 95.4%; Score 1065; DB 4; Length 225;
Best Local Similarity 98.5%; Pred. No. 1.2e-86;
Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDINKDIIGG 66
DB 14 GVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDINKDIIGG 73
QY 67 VLKGGYFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIIGGDLSTLA 126
DB 74 VLKGGYFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIIGGDLSTLA 133
QY 127 GKNFLIVEDVVGTRTKMALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAGFEIPLH 186
DB 134 GKNFLIVEDVVGTRTKMALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAGFEIPLN 193
QY 187 FVVGALDYNEFRDLNHICVINEHG 212
DB 194 FVVGALDYNEFRDLNHICVINEHG 219

RESULT 2
Q60466
ID Q60466 PRELIMINARY; PRT; 218 AA.
AC Q60466;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine (Guanine) phosphoribosyltransferase.
GN HPT.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V79;
RX MEDLINE=93313862; PubMed=8324741;
RA Wei S.J.C., Chang R.L., Bhachech N., Cui X.X., Merkler K.A.,
RA Wong C.O., Hennig E., Yagi H., Jerina D.M., Conney A.H.;
RT "Dose-dependent differences in the profile of mutations induced by
RT (+)-7R,8S-Dihydroxy-9S,10R-epoxy-7,8,9,10-tetrahydrobenzo-(a) pyrene
RT in the coding region of the Hypoxanthine (Guanine)
RT Phosphoribosyltransferase gene in chinese hamster V-79 cells.";
RL Cancer Res. 53:3294-3301(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=V79;
RA Wei S.C.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DB EMBL; X59652; CAA42198.1; -.
DB HSSP; P00492; 1BZY
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Glycosyltransferase, Transferase.
SQ SEQUENCE 218 AA; 24627 MW; 319A7A76992B750D CRC64;
Query Match 70.4%; Score 786; DB 11; Length 218;
Best Local Similarity 69.3%; Pred. No. 6.8e-62;
Matches 147; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

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QY 1 MATRSPGVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDINKDIIGG 60
DB 1 MATRSPSVVISDDEPGYDLDFCIPNHYVEDEKVFIPHGIVIMDRTERLARDVNMKGEGH 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIIGG 120
DB 61 HIVALCVLKGGYKFCADLVEHLKNIISNSDRSIPMTVDYFIRLKSRYNDQSGTDIKVIGGD 120
QY 121 DLSTLAGKNFLIVEDVVGTRTKMALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIIDTGKTMQTLISLVKRYNPKMKVVASLLVVKRTSRSGVGRPDFVG 180
QY 181 FEIPLHFVVGALDYNEFRDLNHICVINEHG 212
DB 181 FEIPDKFVVGALDYNEFRDLNHICVISETG 212

RESULT 3
Q99KF5
ID Q99KF5 PRELIMINARY; PRT; 218 AA.
AC Q99KF5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine guanine phosphoribosyl transferase.
GN HPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DB EMBL; BC004686; AA04686.1; -.
DB HSSP; P00492; 1HMP.
DR MGD; MGI:96217; Hprt.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Glycosyltransferase, Transferase.
SQ SEQUENCE 218 AA; 24544 MW; 83F6DA7507787FA4 CRC64;
Query Match 70.1%; Score 782; DB 11; Length 218;
Best Local Similarity 68.9%; Pred. No. 1.5e-61;
Matches 146; Conservative 31; Mismatches 35; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNLFYTPQHYGDLVYLPHGIIIVDRIERLAKDINKDIIGG 60
DB 1 MATRSPSVVISDDEPGYDLDFCIPNHYAEDEKVFIPHGILIMDRTERLARDVNMKGEGH 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIIGG 120
DB 61 HIVALCVLKGGYKFCADLVEHLKNIISNSDRSIPMTVDYFIRLKSRYNDQSGTDIKVIGGD 120
QY 121 DLSTLAGKNFLIVEDVVGTRTKMALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIIDTGKTMQTLISLVKQYSPKMKVVASLLVVKRTSRSGVGRPDFVG 180
QY 181 FEIPLHFVVGALDYNEFRDLNHICVINEHG 212
DB 181 FEIPDKFVVGALDYNEFRDLNHICVISETG 212

RESULT 4
Q64401
ID Q64401 PRELIMINARY; PRT; 218 AA.

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AC Q64401;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine guanine phosphoribosyltransferase (EC 2.4.2.8).
GN HPT.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Rossiter F., Muzny M., Caskey T., Fox M.;
RT "A Chinese hamster HPRT point mutation reverts to the wild-type
RT sequence.";
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X17656; CRA35648.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR Glycosyltransferase; Transferase.
KW SEQUENCE 218 AA; 24569 MW; A2A97A74P6D6E762 CRC64;

Query Match 69.8%; Score 779; DB 11; Length 218;
Best Local Similarity 68.9%; Pred. No. 2.8e-61;
Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATSPGVIMDDPGYDLNLFYPOHYGDLVLEYPHGIIVDRIERLAKDIMKDIYS 60
Db 1 MATSPSVISDDEFGYDLDFCIPNHYVELEKVFIEPHGIMDRTERLARDVVKMGH 60

Qy 61 DIMVLVCKGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSRYNDQSMGEWQIIGG 120
Db 61 HIVALCVLKGKYPFADLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVI 120

Qy 121 DLSTLAGNFLIVDVGTGTMTKALLSNIKYPKNMKIVASLLVKRTSRSDGFRPDYAG 180
Db 121 DLSTLTGNVLIVEGIIDTGTMTQTLISLVKQYNPKVKVASLLVKRTSRSGVYRDP 180

Qy 181 FEIPLHFLVGVGALDYNEFRDLNHCIVNEHG 212
Db 181 FEIPDKFVGVGALDYNEFRDLNHCIVSETG 212

RESULT 5
Q9JK76 PRELIMINARY; PRT; 210 AA.
AC Q9JK76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
GN HPT.
OS Akodon cursor.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Akodon.
OX NCBI_TaxID=29096;
RN [1]
RP SEQUENCE FROM N.A.
RA Bonvicino C.R.B., Moreira M.A.M., Arcuri R.A., Seunanez H.N.;
RT "Induction and Characterization of Hypoxanthine
RT Phosphoribosyltransferase (hprt) Deficient Cell Lines of Akodon
RT cursor.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF254383; AAF70286.1; -.
DR HSSP; P00492; 1B2Y.

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DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR Pfam; PF00156; PriBosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 210 AA; 23827 MW; CFE3D9270E8048AB CRC64;

Query Match 66.8%; Score 746; DB 11; Length 210;
Best Local Similarity 68.1%; Pred. No. 2.3e-58;
Matches 139; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

Qy 9 VIMDDWPGYDLNLFYPOHYGDLVLEYPHGIIVDRIERLAKDIMKDIYS 68
Db 1 VISDDPGYDLDFCIPNHYIEDLEKVFIEPHGLIMDRTERLARDVVKMGHIIVALCVL 60

Qy 69 KGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSRYNDQSMGEWQIIGGDLSTLACK 128
Db 61 KGGYKFFTDLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGGDDLSTLACK 120

Qy 129 NFLIVEDVVGTRMTKALLSNIKYPKNMKIVASLLVKRTSRSDGFRPDYAGFEIPLHFLV 188
Db 121 NVLIVEDIIDTGTMTQTLISLVKQYNPKVKVASLLVKRTSRSGVYRDPFVGFEIPDKFV 180

Qy 189 VGYALDYNEFRDLNHCIVNEHG 212
Db 181 VGYALDYNEFRDLNHCIVSETG 204

RESULT 6
Q9GJT9 PRELIMINARY; PRT; 186 AA.
AC Q9GJT9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
GN HPRT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-23 FROM N.A.
RC TISSUE=Liver;
RA Poloumienko A., Blecher S.R.;
RT "Exon-intron structure of mammalian HPRT genes.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Poloumienko A., Blecher S.;
RT "Intron-exon structure of bovine and swine HPRT genes.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF294360; AAG18424.1; -.
DR EMBL; AF294354; AAG18424.1; JOINED.
DR EMBL; AF294355; AAG18424.1; JOINED.
DR EMBL; AF294356; AAG18424.1; JOINED.
DR EMBL; AF294357; AAG18424.1; JOINED.
DR EMBL; AF294358; AAG18424.1; JOINED.
DR EMBL; AF294359; AAG18424.1; JOINED.
DR EMBL; AF176419; AAG09236.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.

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DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 186
SQ SEQUENCE 186 AA; 20993 MW; 546486338FC42865 CRC64;

Query Match
Best Local Similarity 59.0%; Score 658; DB 6; Length 186;
Matches 121; Conservative 32; Mismatches 33; Indels 0; Gaps 0;

Qy 15 PGYDLNLFTYQHYXGDLVLYLPHGIIVDRERLAKDIMKDIGYSDIMVLVCKGGYKF 74
Db 1 PGYDLNLFCIPNHNAAEDLEKVFIPHGLIMDRTERLARDVMKEMGGHHIVALCALKGGYKF 60
Qy 75 CADLVEHLKNISSRSDRFVSMKVDPIRLKSYRNDQSGEMQIIGGGDLSTLAGKNFLIVE 134
Db 61 FADLLDYIKALNRNSDRKSIPMTVDPIRLKSYCNDQSTGDIKVIIGGDLSTLTGKNVLIVE 120
Qy 135 DVVGTGRTMKALLSNIKYKPNMKIVASLLVKRTRSRSDGPRPDYAGFPIPHLFVVGVALD 194
Db 121 DIIDTGTMTQTLALVKKHKPMKVASLLMKRTPRSVGYKPDFVGFPIPKFVVVGVALD 180
Qy 195 YNEYFR 200
Db 181 YNEYSR 186

RESULT 7
Q9JK75 PRELIMINARY; PRT; 161 AA.
AC Q9JK75
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mutant hypoxanthine phosphoribosyltransferase (Fragment).
GN HPRT.
OS Akodon cursor.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Akodon.
OX NCBI_TaxID=29096;
EN [1]
FP SEQUENCE FROM N.A.
RA Bonvicino C.R.B., Moreira M.A.M., Arcuri R.A., Seunarez H.N.;
RT "Induction and Characterization of Hypoxanthine
RT Phosphoribosyltransferase (hppt) Deficient Cell Lines of Akodon
RT cursor.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF254384; AAF70287.1; -.
DR HSSP; P00492; 1BZY.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_ip_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; PriBosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPrtase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 161 AA; 18153 MW; FE8305EAF248EF17 CRC64;

Query Match
Best Local Similarity 49.6%; Score 553; DB 11; Length 161;
Matches 104; Conservative 27; Mismatches 30; Indels 0; Gaps 0;

Qy 9 VIMDDWPGYDNLFTYPOHYXGDLVLYLPHGIIVDRERLAKDIMKDIGYSDIMVLVCL 68
Db 1 VISDEPGYDLDLCIPNHYIEDLEKVFIPHGLIMDRTERLARDVMKEMGGHHIVALCVL 60
Qy 69 KGGYKFCADLVEHLKNISSRSDRFVSMKVDPIRLKSYRNDQSGEMQIIGGGDLSTLAGK 128
Db 61 KGGYKFFTDLLDYIKALNRNSDRSIPMTVDPIRLKSYCNDQSTGDIKVIIGGDLSTLTGK 120
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Qy 129 NFLIVEDVVGTRTMKALLSNIKYKPNMKIVASLLVKRTRSRSDGPRPDYAGFPIPHLFVVGVALD 169
Db 121 NVLVEDIIDTGTMTQTLALVKKHKPMKVASLLMKRTPRSVGYKPDFVGFPIPKFVVVGVALD 161

RESULT 8
O46381 PRELIMINARY; PRT; 154 AA.
ID O46381
AC O46381
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
EN [1]
FP SEQUENCE FROM N.A.
RA Boykiw R.H., Sciore P., Reno C., Marchuk L., Frank C.B., Hart D.A.;
RT "Cloning, sequencing, and expression of extracellular matrix molecules
RT in normal and healing rabbit rabbit ligament by RT-PCR.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF020294; AAB87864.1; -.
DR HSSP; P00492; 1HMP.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_ip_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; PriBosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPrtase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 154 AA; 17326 MW; FDBD6F796DF07B2A CRC64;

Query Match
Best Local Similarity 48.7%; Score 543; DB 6; Length 154;
Matches 102; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

Qy 42 IVDRIERLAKDIMKDIGYSDIMVLVCKGGYKFCADLVEHLKNISSRSDRFVSMKVDPIR 101
Db 1 IMDRTERLARDVMKEMGGHHIVALCVLKGKYKFPADLLDYIKALNRNSDRSIPMTVDPIR 60
Qy 102 LKSYRNDQSGEMQIIGGGDLSTLAGKNFLIVEDVVGTRTMKALLSNIKYKPNMKIVA 161
Db 61 LKSYCNDQSTGDIKVIIGGDLSTLTGKNVLIVEDIIDTGTMTQTLALVKKHKPMKVASLLMKRTPRSVGYKPDFVGFPIPKFVVVGVALD 154
Qy 162 SLLVKTRSRSDGPRPDYAGFPIPHLFVVGVALDY 195
Db 121 SLLVKTRPRSVGYRPDFVGFPIPKFVVVGVALDY 154

RESULT 9
Q9XS14 PRELIMINARY; PRT; 142 AA.
ID Q9XS14
AC Q9XS14
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
EN [1]
FP SEQUENCE FROM N.A.
RA Gyoerify A., Steinborn R., Baiaesch M., Plana-Duran J., Klein D.,
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RA Mueller M., Brem G.;
RL "Variant pPRT sequence.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF143818; AAD30159.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR002375; Pf/PY_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Priboyltran; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 142
FT NON_TER 142
SQ SEQUENCE 142 AA; 15365 MW; 4FA8CEB7D25F4983 CRC64;

Query Match 42.1%; Score 470; DB 6; Length 142;
Best Local Similarity 61.3%; Pred. No. 4.5e-34;
Matches 87; Conservative 28; Mismatches 27; Indels 0; Gaps 0;

QY 20 NLFTYPOHYGDLEVLPHGIIIVDRIBRLAKDINKDIGSDIMVLCVKGKGFADLV 79
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DLFCIPHYAEDLEKVFIPHGLIMDRTERLARDVMKGGHHIVALCVLKGKGFADLL 60
QY 80 EHLKNJSRNSDRFVSMKVDFTRLKSYRNDQSMGEMQIIGGDLSTLACKNFIIVDVG 139
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 DYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGGDLSTLTKNVLIVEDI 120

QY 140 GRTMKALLSNIIEKYKPNMKVA 161
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 GKTWTLLSLVKQHNPKMKVA 142

RESULT 10
ID Q28968 PRELIMINARY; PRT; 135 AA.
AC Q28968;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
GN HPRT.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; U32316; AAB03248.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pf/PY_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Priboyltran; 1.
DR TIGRfams; TIGR01203; HGPRase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 135
FT NON_TER 135
SQ SEQUENCE 135 AA; 15017 MW; E758F6B0B090F9A09 CRC64;

Query Match 40.9%; Score 456; DB 6; Length 135;
Best Local Similarity 63.0%; Pred. No. 7.5e-33;
Matches 85; Conservative 27; Mismatches 23; Indels 0; Gaps 0;

QY 47 ERLAKDTMKDIGSDIMVLCVKGKGFADLVHLKNISNRNSDRFVSMKVDFTIRLKS 106
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ERLARDVMKGGHHIVALCVLKGKGFADLLDYIKALNRNSDTSIPMTVDFIRLKS 60
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QY 107 NDQSMGEMQIIGGDLSTLACKNFIIVDVGVTGRTMKALLSNIIEKYKPNMKVASLLVK 166
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 NDQSTGDIKVIIGGDLSTLTKGNVLIVEDIIDTGTMTQTLTLVLKQHNPKMKVASLLVK 120

QY 167 RTSRSDGFRPDYAGF 181
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 RTPRSVGYRPFVGF 135

RESULT 11
ID Q28530 PRELIMINARY; PRT; 193 AA.
AC Q28530; Q29493;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)
DE Hypoxanthine phosphoribosyltransferase (HGPase) (IMP pyrophosphorylase)
DE guanine phosphoribosyltransferase (TRANSPHOSPHORIBOSIDASE) (Guanine phosphoribosyltransferase)
DE (Fragment).
GN HPRT.
OS Macropus robustus (Wallaroo) (Euro).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9319;
RN [1]
RP SEQUENCE FROM N.A.
RA Conaty J., Piper A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 166-187 FROM N.A.
RX MEDLINE=93289446; PubMed=7685549;
RA Piper A.A., Bennett A.M., Noyce L., Swanton M.K., Cooper D.W.;
RL "Isolation of a clone partially encoding hill kangaroo X-linked
RT hypoxanthine phosphoribosyltransferase: sex differences in methylation
RT in the body of the gene.";
RL Somat. Cell Mol. Genet. 19:141-159(1993).
CC -!- CATALYTIC ACTIVITY: IMP + DIPHOSPHATE = HYPOXANTHINE + 5-PHOSPHO-
CC ALPHA-D-RIBOSE 1-DIPHOSPHATE.
DR EMBL; L41993; AAA81355.1; -.
DR EMBL; M77683; AAA31600.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Priboyltran; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 193
FT NON_TER 193
SQ SEQUENCE 193 AA; 21153 MW; 2C1DA5037FA5F010 CRC64;

Query Match 40.8%; Score 455; DB 6; Length 193;
Best Local Similarity 64.2%; Pred. No. 1.5e-32;
Matches 86; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 1 MATSPGVIMDDWPGVDLNLFTYPQHYGDLVLPVPHGIIIVDRIBRLAKDINKDIGS 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 MANLSPSIVIEDDEPGYDLDFCIPKHYAQDLKVFIPHGLIMDRTERLARDVMKGGH 119

QY 61 DIMVLCVKGKGFADLVHLKNISNRNSDRFVSMKVDFTIRLKSYNRNDQSMGEMQIIGG 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 HIVALCVLKGKGFADLLDYIKALNRNSDKSIPMTVDFIRLKSVCNDQSTGDIKVIIG 179

QY 121 DLSTLACKNFIIV 134
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
180 DLSTLTKGNVLIV 193

RESULT 12
ID O96085 PRELIMINARY; PRT; 231 AA.
AC O96085;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
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```
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyl transferase (HGPRt).
GN HGPRt.
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XAT;
RX MEDLINE=21165804; PubMed=11269277;
RA Onda T., Miyamoto K., Sugioke Y., Kangawa K., Kano S., Suzuki M.;
RT "Suppressed expression of hypoxanthine-guanine
RT phosphoribosyltransferase (HGPRt) in an irradiation-attenuated
RT Plasmodium berghei XAT strain.";
RL Parasitol. Int. 48:157-167(1999).
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AB020413; BAA34691.1; -.
DR HSSP; P20035; 1CJB.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRfams; TIGR01203; HGPRtase; 1.
DR PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 231 AA; 26525 MW; C028F5E45CDB8B72 CRC64;

Query Match 40.0%; Score 446.5; DB 5; Length 231;
Best Local Similarity 42.7%; Pred. No. 1.1e-31;
Matches 91; Conservative 41; Mismatches 66; Indels 15; Gaps 4;

Qy 8 VVIMDDWPGYDNLNFTYPQHYGYDLEYVLIIPHGIIVDRIERLAKDIMKDIKCV 67
Dy 17 VMIKDD-DGVEFDSFVTPDHYKNVLRILIPNGLIKSRVERMAFDISRTYNGEFLHLL 75
Qy 68 LKGGYKFCADLVEHLKNI-----SRNSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGG 119
Dy 76 LKGRSFRFTSLKLDLRHNYVIADASTNSR-----BHYVRVKSVCNTQSTGRLEIV-S 129
Qy 120 GDLSTLAGKNFLIVEDVVGTRTMKALLSNIEKYKPNMKIVASLLVKRTSRSDGFRP 179
Dy 130 EDLSCLGKGNLIVEDIIDTGNLTLSKFCDYLLKKFEKPTIAVSALYIKETPLWNGFKAD 189
Qy 180 GFEIPLHFLVGVGYALDNEYFRDLNHCIVINEHG 212
Dy 190 GFSVENPFLVGCGLDYNENFRDLNHCIVINEHG 222

RESULT 13
ID Q81J51 PRELIMINARY; PRT; 231 AA.
AC Q81J51
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypoxanthine phosphoribosyltransferase.
GN Pf10_0121.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perteira M., Allen J., Selegut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014830; AAN35319.1; -.
KW Transferase; Glycosyltransferase..
SQ SEQUENCE 231 AA; 26362 MW; BC6D3B30486DD287 CRC64;

Query Match 39.9%; Score 445.5; DB 5; Length 231;
Best Local Similarity 42.7%; Pred. No. 1.3e-31;
Matches 93; Conservative 40; Mismatches 74; Indels 11; Gaps 3;

Qy 5 SPGV-----VIMDDWPGYDNLNFTYPQHYGYDLEYVLIIPHGIIVDRIERLAKDIMKDI 57
Dy 6 NPGAGENAFDFVFKDDGDDYDLSFMIPAHYKYLTKLVLPNGVGNRIEKLAYDIKKVY 65
Qy 58 GYSIDIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKV--DFIRLKSRYNDQSMGEM 114
Dy 66 NNEEFHILCLLKGSRGFTALLKLSRIHNSAVETSAPLFGHEHYVRVKSVCNDQSTGTL 125
Qy 115 QIIIGGDLSTLAGKNFLIVEDVVGTRTMKALLSNIEKYKPNMKIVASLLVKRTSRSDGF 174
Dy 126 EIV-SEDLSCCLKGKHLVIEDIIDTKTLVKFCEVKKFEIKTVAIAICLFIKRTPLWNGF 184
Qy 175 RPYAGFEIPLHFLVGVGYALDNEYFRDLNHCIVINEHG 212
Dy 185 KADFVGFSPDHPFVGVGYSLDYNIEFRDLNHCIVINEHG 222

RESULT 14
Q95258 PRELIMINARY; PRT; 136 AA.
ID Q95258
AC Q95258;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
GN HPRT.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Mansfield L.;
RT "Porcine HPRT sequence.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; U69731; AAB16389.1; -.
DR HSSP; P00492; 1HMP.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 136
SQ SEQUENCE 136 AA; 15399 MW; D531783C182A1FF7 CRC64;

Query Match 39.2%; Score 437; DB 6; Length 136;
Best Local Similarity 63.1%; Pred. No. 3.7e-31;
Matches 82; Conservative 26; Mismatches 22; Indels 0; Gaps 0;

Qy 47 ERLAKDIMKDIKCVLIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKSRY 106
Dy 1 ERLARDVWKEMGGHHIIVALCVLKGYYFADLLDIYIKALNNSDRSPMTVDVDFRLKSYC 60
Qy 107 NDQSMGEMQIIGGDLSTLAGKNFLIVEDVVGTRTMKALLSNIEKYKPNMKIVASLLVK 166
Dy 61 NDQSTGDIKVIIGGDLSTLAGKNFLIVEDIIDTKTMQTLTLLSLVKQHPKMKVASLLVK 120
Qy 167 RTSRSDGFRP 176
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OM protein - nucleic search, using frame_plus_p2n model
Run on: October 4, 2003, 12:13:13 ; Search time 2584 Seconds
(without alignments)
3356.363 Million cell updates/sec

Title: US-09-902-705-2
Perfect score: 1116
Sequence: 1 MATRSPGVIMDDPCYDIN.....LDYNEYPDLNHICVINEHG 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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- 18: em_in:*
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- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
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- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
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- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1069	95.8	1927	6	AR310478	AR310478 Sequence
2	1065	95.4	807	9	AF226056	AF226056 Homo sapi
3	1065	95.4	1450	9	BC008662	BC008662 Homo sapi
4	1065	95.4	1926	6	BD159230	BD159230 Primer fo
5	1065	95.4	1926	9	AK021950	AK021950 Homo sapi
6	1038	93.0	783	6	BD146172	BD146172 Primer fo
7	786	70.4	657	10	CLHPRT	X59652 C. longicau
8	783	70.2	702	10	MUSHPRTS	M20011 Mus spretus
9	782	70.1	1281	10	BC004686	BC004686 Mus muscu
10	779	69.8	685	9	S43335	S43335 hprt=hypoxa
11	779	69.8	1222	10	CLHPRTM	X17656 C.longicaud
12	779	69.8	1316	9	BC000578	BC000578 Homo sapi
13	779	69.8	1331	9	HSHPRT	V00530 Human mRNA
14	779	69.8	1331	9	HUMHPT	M31642 Human hypox
15	776	69.5	1301	10	CRUHPRT	J00060 Chinese ham
16	776	69.5	1303	10	MERHPRT	L37778 Meriones un

17 775 69.4 654 9 HUMHPRTD
 18 772 69.2 654 9 HUMHPRTC
 19 772 69.2 1289 6 AR016505 Sequence
 20 772 69.2 1289 6 AR096888 Sequence
 21 772 69.2 1289 6 HD136083 Sequence
 22 772 69.2 1289 10 MUSHPT
 23 768.5 68.9 5247 6 AR215116 Sequence
 24 768.5 68.9 5247 6 AR302358 Sequence
 25 768.5 68.9 5314 6 AR215123 Sequence
 26 768.5 68.9 5314 6 AR302365 Sequence
 27 768 68.8 853 10 RATHPT
 28 768 68.8 853 10 S79292
 29 768 68.8 1144 10 RHPRPT
 30 762 68.3 1724 5 BC046003 Danio rer
 31 753 67.5 1545 5 GGN132697
 32 746 66.8 729 10 AF254383
 33 737 66.0 729 10 AF254384
 34 721 64.6 2867 4 WALHPT
 35 716 64.2 1316 5 BC047173
 36 672 60.2 407 6 AX071321
 37 658 59.0 558 4 AF176419
 38 611 54.7 8157 2 AL831743
 39 609 54.6 5482 12 AF090455
 40 609 54.6 5581 6 BD094704
 41 599.5 53.7 110000 2 AC123419.2
 42 599.5 53.7 246199 2 AC127759
 43 599.5 53.7 313691 2 AC096152
 44 571 51.2 654 6 AX526038
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ALIGNMENTS

RESULT 1
 AR310478 1927 bp DNA linear PAT 12-JUN-2003
 LOCUS
 DEFINITION Sequence 19 from patent US 6558935.
 ACCESSION AR310478
 VERSION AR310478.1 GI:31703441
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

UNCLASSIFIED.
 1 (bases 1 to 1927)
 TANG Y.T., CORLEY N.C., GUEGLER K.J., BAUGHN M.R., LAL P., YUE H.,
 HILLMAN J.L. and AZIMZAI Y.
 Human transferase proteins
 Patent: US 6558935-A 19 06-MAY-2003;
 Location/Qualifiers
 source
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 ORIGIN

Alignment Scores:
 Pred. No.: 1.11e-106 Length: 1927
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 Qy 27 HisTyrTyrGlyAspLeuGluTyrValLeuIleProHisGlyIleIleValAspArgIle 46
 Db 118 CACTATTATGAGACATTTGGAGTATGCTCTCATCCCTCATGCTATCATTTGTCGACAGAAT 177
 Qy 47 GluAsnLeuAlaLysAspIleMetLysAspIleGlyTyrSerAspIleMetValLeuCys 66
 Db 178 GAGCGCTGGCCAGGATATTATGAGACATAGATATAGTACATCATGCTCTGTGT 237
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 Qy 107 AsnAspGlnSerMetGlyGluMetGlnIleIleGlyGlyAspLeuSerThrIleAla 126
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 Qy 167 ArgThrSerArgSerAspGlyPheArgProAspTyrAlaGlyPheGluIleProHisLeu 186
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 Qy 187 PheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArgAspLeuAsnHisIleCys 206
 Db 598 TTTGTGCTGGGATGCTTATGATTACAAATGATACTTACAGAGATCTGATCACAATATGC 657
 Qy 207 ValIleAsnGluHisGly 212
 Db 658 GTCATCATGAGCAGCGGT 675
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 LOCUS
 DEFINITION Homo sapiens HHGP (HHGP) mRNA, complete cds.
 ACCESSION AF226056
 VERSION AF226056.1 GI:9295350

KEYWORDS	FLI_CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 807)
AUTHORS	Li Y., Wu T., Xu S., Ren S., Chen Z. and Han Z.
TITLE	A novel gene expressed in human liver cancer tissue
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 807)
AUTHORS	Li Y., Wu T., Xu S., Ren S., Chen Z. and Han Z.
TITLE	Direct Submission
JOURNAL	Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
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ORIGIN	
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Pred. No.:	9.13e-107 Length: 807
Score:	1065.00 Matches: 203
Percent Similarity:	99.03% Conservative: 1
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Query Match:	95.43% Indels: 0
DB:	9 Gaps: 0
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QY	47 GluArgLeuAlaIlyAspIleMetIlyAspIleGlyTyrSerAspIleMetValLeuCys 66

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QY	167	ArgThrSerArgSerAspGlyPheArgProAspTyrAlaGlyPheGluLleProHisLeu186
Db	549	AGAACATCCAGAGTGCAGCGCTTTAGACCTGACTACTCTGGATTGAGATTCAAACTTA608
QY	187	PheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArgAspLeuAsnHisIleCys206
Db	609	TTTGTGGGATATCCCTTAGATTACAAATGAATACATTGAGAGATCTGAATCAATATGC668
QY	207	ValIleAsnGluHisGly212
Db	669	GTCATCATGAGCACGGT686
RESULT 5		
AK021950		
LOCUS		
DEFINITION	Hommo sapiens cDNA FLJ11888 fis, clone HEMBA1007243, weakly similar to Chinese hamster hprt mRNA.	mRNA linear PRI 01-AUG-2002
ACCESSION	AK021950	
VERSION	AK021950.1	GI:10433254
KEYWORDS	oligo capping; fis (full insert sequence).	
SOURCE	Hommo sapiens (human)	
ORGANISM	Hommo sapiens	
REFERENCE		
AUTHORS	1 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arta,M., Nabeкура,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.	NEO human cDNA sequencing project
TITLE	Unpublished	
REFERENCE	2 (bases 1 to 1926)	
AUTHORS	Isogai,T. and Otsuki,T.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomic@helix.co.jp, tel:81-438-52-3975, fax:81-438-52-3986)	
COMMENT	NEO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology and clone library construction, 5'- & 3'-end one pass sequencing and clone selection Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.	
FEATURES		
source	Location/Qualifiers	
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	/tissue_type="whole embryo, mainly head"	

Percent Similarity: 98.54% Conservatives: 1
 Best Local Similarity: 98.05% Mismatches: 2
 Query Match: 93.01% Indels: 1
 DB: 6 Gaps: 0

US-09-902-705-2 (1-212) x BD146172 (1-783)

QY 7 GlyValValIleMetAspTyrProGlyTyrAspLeuAsnLeuPheThrTyrProGln 26
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 Db 69 GCGTCTGCTGATTATGATGATGGCCAGGATGACTTGAATTATTACGTACCCACAG 128
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QY 27 HisTyrTyrGlyAspLeuGluTyrValLeuIleProHisGlyIleValaspArgIle 46
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 Db 129 CACTATTATGAGACTTGGAGTATGCTCTCATCCTCATGCTATCATTTGGACAGATT 188
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QY 47 GluArgLeuAlaLysAspIleMetLysAspIleGlyTyrSerAspIleMetValLeuCys 66
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 Db 189 GAGCGGCTGCCAGGATATTATGAAGACATAGGATATAGTCATCATGCTGCTGTGT 248
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QY 87 ArgAsnSerAspArgPheValSerMetLysValaspPheIleArgLeuLysSerTyrArg 106
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 Db 309 CGAAATTCAGATCGATTGTCTCAATGAAGGTTGATTTTCATCAGACTAAAAGTTACAGG 368
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QY 107 AsnAspGlnSerMetGlyGluMetGlnIleIleGlyGlyAspLeuSerThrLeuAla 126
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 Db 369 AATGACAGCTCCATGGTGAGATGACGATAATCGAGGCGATGATCTTCAACGCTGCT 428
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QY 127 GlyLysAsnPheLeuIleValGluAspValValGlyThrGlyArgThrMetLysAlaLeu 146
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 Db 429 GAAAGAGATGTTCTCATGTGTGAGATGTCTCGAACTGGGAGGACCATGAAGCACTA 488
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QY 147 LeuSerAsnIleGluLysTyrLysProAsnMetIleLysValAlaSerLeuLeuValLys 166
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 Db 489 CTCAGCAATATAGAGTAATACAGCCCAACATGATTAAGTAGCCAGTTTGTGTGAG 548
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QY 167 ArgThrSerArgSerAspGlyPheArgProAspTyrAlaGlyPheGluIleProHisLeu 186
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 Db 549 AGAACATCCAGAGTGCAGCGCTTTAGACCTGACTATGCTGGATTTGAGATTCCAAACTA 608
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QY 187 PheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArgAspLeuAsnHisIleCys 206
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QY 207 -ValIleAsnGlu 210
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Db 669 CGTCATCAATGAG 681
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RESULT 7
 CLHPRT
 LOCUS
 DEFINITION
 C. longicaudatus hprt mRNA for hypoxanthine (guanine)
 phosphoribosyltransferase.
 X59652

VERSION X59652.1 GI:461343
 KEYWORDS hprt gene; mutant.
 SOURCE Cricetulus longicaudatus (long-tailed hamster)
 ORGANISM Cricetulus longicaudatus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 Cricetulus.

REFERENCE 1
 AUTHORS Wei, S.J., Chang, R.L., Bhachech, N., Cui, X.X., Merkler, K.A.,
 Wong, C.Q., Hennig, E., Yagi, H., Jerina, D.M. and Conney, A.H.
 TITLE Dose-dependent differences in the profile of mutations induced by
 (+)-7R,8S-dihydroxy-9S,10R-epoxy-7,8,9,10-tetrahydrobenzo(a)pyrene
 in the coding region of the hypoxanthine (guanine)
 phosphoribosyltransferase gene in Chinese hamster V-79 cells
 JOURNAL Cancer Res. 53 (14), 3294-3301 (1993)
 MEDLINE 93313862
 PUBMED 8324741

REFERENCE 2 (bases 1 to 657)
 AUTHORS Wei, S.C.
 TITLE Direct Submission
 JOURNAL Submitted (08-FEB-1994) S.C. Wei, Rutgers The State University,
 College of Pharmacy, Laboratory for Cancer Research, Dept of
 Chemical Biology & Pharmacognosy, Piscataway NJ 08855, USA

FEATURES
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BASE COUNT 193 a 114 c 161 g 189 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.85e-76 Length: 657
 Score: 786.00 Matches: 147
 Percent Similarity: 83.49% Conservatives: 30
 Best Local Similarity: 69.34% Mismatches: 35
 Query Match: 70.43% Indels: 0
 DB: 10 Gaps: 0

US-09-902-705-2 (1-212) x CLHPRT (1-657)

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RESULT 8
MUSHPTS
LOCUS MUSHPTS 702 bp mRNA linear ROD 02-APR-1996
DEFINITION Mus spretus hypoxanthine phosphoribosyltransferase mRNA, 5' end.
ACCESSION M20011
VERSION M20011.1 GI:194000
KEYWORDS hypoxanthine phosphoribosyltransferase.
SOURCE Mus spretus (western wild mouse)
ORGANISM Mus spretus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 702)

1 MetAlaThrArgSerProGlyValValIleMetAspTyrProGlyTyrAspLeuAsn 20
QY

RESULT	9
BC004686	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	

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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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(clonal) outgrowth infected with the virus MMTV."

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62. 718

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BASE COUNT 380 a 230 c 272 g 399 t

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-75 Length: 1281

Score: 782.00 Matches: 146

Percent Similarity: 81.49% Conservative: 31

Best Local Similarity: 68.87% Mismatches: 35

Query Match: 70.07% Indels: 0

DB: 10 Gaps: 0

US-09-902-705-2 (1-212) x BC004686 (1-1281)

Qy 1 MetAlaThrArgSerProGlyValValIleMetAspTyrProGlyTyrAspLeuAsn 20

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Qy 21 LeuPheThrTyrProGlnHisTyrTyrGlyAspLeuGluTyrValLeuIleProHisGly 40

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Db CACATTGGCCCTCTGTGTGCTCAAGGGGGGCTATAAGTCTTGTGACCTGTGGAT 301

Qy 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle 100

Db TACATTAAAGCAGCTAGTAAATAGTATAGATCCATTCCTATGACTGTAGATTATC 361

Qy 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyCyluMetGlnIleIleGlyGly 120

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Qy 181 PheGluIleProHisLeuPheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArg 200

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Db GATTTCGAATCAGTGTGTTGTCATTAGTCAAACTGGA 697

RESULT 10

S43335

LOCUS S43335 685 bp mRNA linear PRI 08-MAY-1993

DEFINITION hprt=hypoxanthine phosphoribosyltransferase [cynomolgus monkeys,

ACCSSION S43335

VERSION S43335.1 GI:254239

KEYWORDS Macaca fascicularis (crab-eating macaque)

SOURCE Macaca fascicularis

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 685)

AUTHORS Harbach,P.R., Filipunas,A.L., Wang,Y. and Aaron,C.S.

TITLE DNA sequence analysis of spontaneous and

Qy N-ethyl-N-nitrosourea-induced hprt mutations arising in vivo in

Db cynomolgus monkey T-lymphocytes

JOURNAL Environ. Mol. Mutagen. 20 (2), 96-105 (1992)

MEDLINE 92371466

PUBMED 1505533

REMARK GenBank staff at the National Library of Medicine created this

entry [NCBI Gibbsq 111886] from the original journal article.

FEATURES

Location/Qualifiers

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BASE COUNT 203 a 114 c 169 g 199 t
ORIGIN

Alignment Scores:
Pred. No.: 1.13e-75 Length: 685
Score: 779.00 Matches: 145
Percent Similarity: 83.02% Conservative: 31
Best Local Similarity: 68.40% Mismatches: 36
Query Watch: 69.80% Indels: 0
DB: 9 Gaps: 0

US-09-902-705-2 (1-212) x S43335 (1-685)

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Db 607 GATTGATCATCTTTGTGTGTCATTAGTGAACCTGGA 642

RESULT 11
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LOCUS C.Longicaudatus HPRT mRNA for hypoxanthine guanine linear ROD 21-MAY-1992
DEFINITION phosphoribosyltransferase.
ACCESSION X17656
VERSION X17656.1 GI:49514
KEYWORDS hprt gene; hypoxanthine-guanine phosphoribosyltransferase; point mutation.
SOURCE Cricetulus longicaudatus (long-tailed hamster)
ORGANISM Cricetulus longicaudatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
REFERENCE 1
AUTHORS Rossiter, F., Muzny, M., Caskey, T. and Fox, M.
TITLE A Chinese hamster HPRT point mutation reverts to the wild-type sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1222)
AUTHORS Rossiter, F.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-1989) Rossiter B. J. F., Institute for Molecular Genetics, Baylor College of Medicine, 1, Baylor Plaza, Houston, Texas 77030, USA
COMMENT See also J00060.
FEATURES
Location/Qualifiers
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variation 420

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Qy	201	AspLeuAsnHisIleCysValIleAsnLHisGly	212
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LOCUS	BC000578	1316 bp	mRNA	linear	PR1 12-JUN-2000
DEFINITION	Homo sapiens, hypoxanthine phosphoribosyltransferase 1 (lesch-Nyhan syndrome), clone MGC:1722 IMAGE:3163726, mRNA, complete cds.				
ACCESSION	BC000578				
VERSION	BC000578.1	GI:12653602			
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1 (bases 1 to 1316)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov Shvetenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C.C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tlionson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

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This clone was selected for full length sequencing because it
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source

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/note="Vector: pOTB7"
49..705
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(lesch-Nyhan syndrome)"
/protein_id="AA00578.1"
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CDS

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BASE COUNT 408 a 215 c 278 g 415 t
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Score: 779.00 Matches: 145
Percent Similarity: 83.02% Conservative: 31
Best Local Similarity: 68.40% Mismatches: 36
Query Match: 69.80% Indels: 0
DB: 9 Gaps: 0

US-09-902-705-2 (1-212) x BC000578 (1-1316)

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Db 49 ATGGCGACCGCAGCCTGGCGTCTGATTAGTATGATGATGAACACGATTATGACCTTAT 108
QY 21 LeuPheThrTyrProGlnHisTyrTyrGlyAspLeuGluTyrValLeuIleProHisGly 40
Db 109 TTAATTGTCATACCTAATCATATTATCTGAGGATTTCGAAAGGGTGTATTCTCTCATGGA 168
QY 41 IleIleValAspArgIleGluArgLeuAlaLysAspIleMetLysAspIleGlyTyrSer 60
Db 169 CTAAATTATGACAGCAGCTGAACCTCTGCTCGAGATGTGATGAAGGAGATGGAGGCCAT 228
QY 61 AspIleMetValLeuCysValLeuLysGlyTyrTyrLysPheCysAlaAspLeuValGlu 80
Db 229 CACATTGTAGCCCTCTGTGCTCTCAGGGGGGCTATAAAATCTTGTCTGACCTGTGGAT 288
QY 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle 100
Db 289 TACATCAAGCACTGAATAGATAGTATGATATCCATTCCTATGACTGTAGATTATATC 348
QY 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyGluMetGlnIleIleGlyGly 120
Db 349 AGACTGAAGAGCTATTGTAATGATACCACTGACACAGGGGACATAAAAGTAATTGTGGAGAT 408
QY 121 AspLeuSerThrLeuAlaGlyLysAsnPheLeuIleValGluAspValValGlyThrGly 140
Db 409 GATCTCTCAACTTTAACTGGAAGAAGATCTTCTGATTGTGGAAGATATAATTGACACTGGC 468

QY 141 ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrLysProAsnMetIleLysVal 160
Db 469 AAACATATGCAGACTTTCCTTCTGTCAGCAGTATAATCCAAAGATGGTCAGATC 528
QY 161 AlaSerLeuLeuValLysArgThrSerArgSerAspGlyPheArgProAspTyrAlaGly 180
Db 529 GCAAGCTTGTCTGTGTAAGAGCACCACCAAGTGTGGATATAAGCCAGACTTTGTGGA 588
QY 181 PheGluIleProHisLeuPheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArg 200
Db 589 TTTGAAATTCACACAAAGTTTGTGTAGGATATCCCTTGACTATAATGATATCTCAGG 648
QY 201 AspLeuAsnHisIleCysValIleAsnGluHisGly 212
Db 649 GATTGATCATGTTTGTGTGTCATTTAGTGAAGACTGGA 684

RESULT 13

HSHPRT

LOCUS HSHPT 1331 bp mRNA linear PRI 02-JUL-1999
DEFINITION Human mRNA encoding IMP:Pyrophosphate phosphoribosyltransferase
E.C. 2.4.2.8.

ACCESSION V00530

VERSION V00530.1 GI:32449

KEYWORDS complementary DNA; transferase.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1331)

AUTHORS Jolly D.J., Okayama H., Berg P., Esty A.C., Filpula D., Bohlen P.,

Johnson G.G., Shively J.E., Hunkapillar, T. and Friedmann, T.

TITLE Isolation and characterization of a full-length expressible cDNA

for human hypoxanthine phosphoribosyl transferase

Proc. Natl. Acad. Sci. U.S.A. 80 (2), 477-481 (1983)

JMOL 83169681

PUBMED 6300847

COMMENT Data kindly reviewed (30-MAY-1983) by D.J. Jolly.

FEATURES

Location/Qualifiers

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BASE COUNT 385 a 237 c 281 g 428 t

ORIGIN

Alignment Scores:									
Pred. No.:	2,84e-75	Length:	1331						
Score:	779.00	Matches:	145						
Percent Similarity:	83.02%	Conservative:	31						
Best Local Similarity:	68.40%	Mismatches:	36						
Query Match:	69.80%	Indels:	0						
DB:	9	Gaps:	0						
US-09-902-705-2 (1-212) x HSHPT (1-1331)									
QY	1	MetaLthrArgSerProGlyValIleMetAspTrpProGlyTyrAspLeuAen	20						
Db	86	ATGGCGACCCGCCCTGGGTGCATTAGTAGATCATCAACAGGTTATGACCTTGAT	145						
QY	21	LeuPheThrTyrrProGlnHisTyrrGlyAspLeuGluTyrrValIleProHisGly	40						
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QY	41	IlelleValAspArgIleGluArgLeuAlaIysAspIleMetIleAspIleGlyTyrSer	60						
Db	206	CATATTATGACGAGACTCAACGCTCTCTCGATGATGATGATGATGATGATGATGAT	265						
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Db	266	CACATTATGACCCTCTGTCTGCTCAAGGGGGCTATAAAATCTTCTGCTGCTGGAT	325						
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QY	121	AspLeuSerThrLeuAlaGlyIysAsnPheLeuIleValGluAspValValGlyThryGly	140						
Db	446	GATCTCTCAACTTAACTGGAAGAATGCTTGTATGTCGGAAGATATAAATGACACTGC	505						
QY	141	ArgThrMetIysAlaLeuLeuSerAnIleGluIysTyrrIysProAsnMetIleIysVal	160						
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Db	626	TTTGAATTCACAGACAGTTGTGTAGGATATGCCCTTGACATATATGATATCTCAGG	685						
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Db	686	GATTGTAATCATGTTGTGTCATTAGTCAAACCTGA	721						
RESULT 14									
HUMHPT	FOCUS	1331 bp	mRNA	linear	PRI	08-NOV-1994			

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Chinese hamster: construction and sequence analysis of cDNA recombinants
JOURNAL Nucleic Acids Res. 10 (21), 6763-6775 (1982)
MEDLINE 83090437
PUBMED 6294614
COMMENT Original source text: Hamster (Chinese, v79) cell line rjkl59 CDNA to mRNA.

Hprt catalyzes vital steps in the reutilization pathway for purine biosynthesis. The hprt gene is known to be x-linked in mammals. A high degree of homology is found between the mouse and hamster nucleotide sequences. See other loci with hprt as the 4th-7th characters in the locus name. Multiple poly-A sites are proposed for the hamster.

FEATURES
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        polyA_signal 1279..1284
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BASE COUNT 369 a 244 c 269 g 419 t
ORIGIN      90 bases 5' to the putative cds start, near a hha-i site.

Alignment Scores:
Pred. No.:   5.84e-75          Length:       1301
Score:       776.00           Matches:       146
Percent Similarity: 83.02%     Conservative:  30
Best Local Similarity: 68.87% Mismatches:       36
Query Match:   69.53%         Indels:         0
DB:            10             Gaps:          0

US-09-902-705-2 (1-212) x CRUHPRT (1-1301)

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QY 21 LeuPheThrTyProClhHisTyrTyrrGlyAspLeuGluTyrValIleProHisGly 40
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QY 41 IlelleValaspArgilleGuaIgLeuAlalysAspileMetLysaspileGlyTyrSer 60

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Db 211 GTGATTATGACAGAGACTGAAAGACTTCCCGAGATGTCTATGAAGAGATGGAGGCCAT 270
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 Db 271 CACATTGTGGCCCTCTGTGCTGAGAGGGGGCTATAAATCTTGTGACCTGTGGAT 330
 QY 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle 100
 Db 331 TACATTAAAGCAGCTGAATAGAAATAGTAGATCCATCCCATGACTGTAGATTTATC 390
 QY 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyGluMetGlnIleIleGlyGly 120
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 Job time : 2590 secs